

91549

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From: Gibbs, Terra
Sent: Tuesday, April 15, 2003 10:47 AM
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Subject: Sequence search request...

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Could you please do a regular search of SEQ ID NO:78 of USSN 09800629?

Please no EST's.

Terra Gibbs #79523
AU 1635
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306-3221

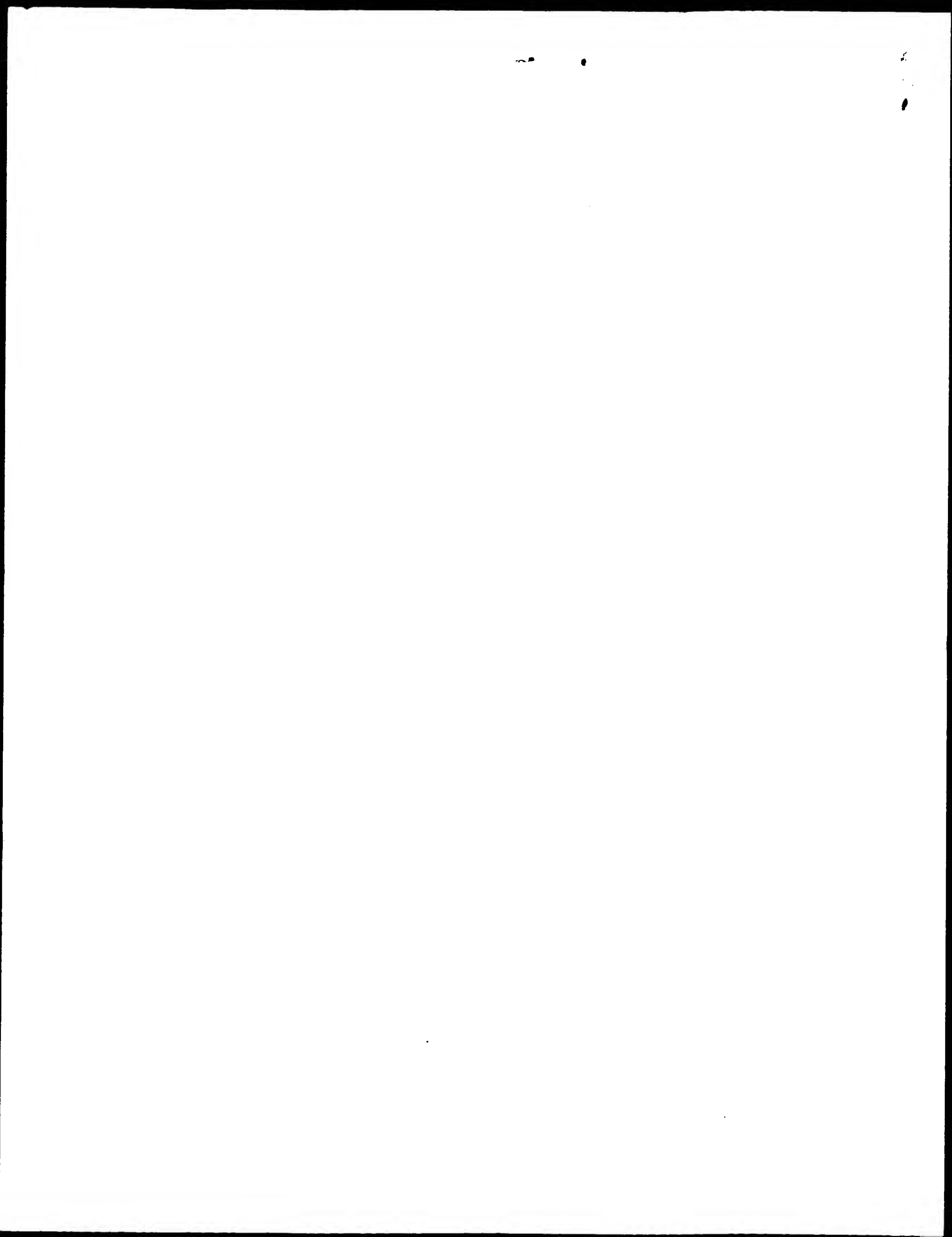
THANK YOU!

POINT OF CONTACT:
PAUL SCHULWITZ
TECHNICAL INFO. SPECIALIST
GM1 6B06 TEL. (703) 305-1954

Searcher: _____
Phone: _____
Location: _____
Date Picked Up: 4/16
Date Completed: 4/24
Searcher Prep/Review: _____
Clerical: _____
Online time: _____

TYPE OF SEARCH:
NA Sequences: _____
AA Sequences: _____
Structures: _____
Bibliographic: _____
Litigation: _____
Full text: _____
Patent Family: _____
Other: _____

VENDOR/COST (where applic.)
STN: _____
DIALOG: _____
Questel/Orbit: _____
DRLink: _____
Lexis/Nexis: _____
Sequence Sys.: _____
WWW/Internet: _____
Other (specify): _____



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OM nucleic - nucleic search, using sw model

Run on: April 23, 2003, 22:52:02 ; Search time 9284 Seconds

(without alignments)
10125.168 Million cell updates/sec

Title: US-09-800-629A-78

Perfect score: 3230

Sequence: 1 atcctaatacaagaccacagc.....aaaactctctcaagatcc 3230

Scoring table: IDENTITY_NUC

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Database : GenEmbl:*

- 1: gb_ba:*
- 2: gb_htg:*
- 3: gb_in:*
- 4: gb_om:*
- 5: gb_ov:*
- 6: gb_pat:*
- 7: gb_ph:*
- 8: gb_pr:*
- 9: gb_ro:*
- 10: gb_sts:*
- 11: gb_sy:*
- 12: gb_un:*
- 13: gb_vi:*
- 14: em_ba:*
- 15: em_fun:*
- 16: em_hum:*
- 17: em_mu:*
- 18: em_ov:*
- 19: em_pat:*
- 20: em_ph:*
- 21: em_pl:*
- 22: em_ro:*
- 23: em_sts:*
- 24: em_sy:*
- 25: em_un:*
- 26: em_vi:*
- 27: em_ba:*
- 28: em_fun:*
- 29: em_hum:*
- 30: em_mu:*
- 31: em_ov:*
- 32: em_pat:*
- 33: em_ph:*
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- 36: em_sts:*
- 37: em_sy:*
- 38: em_un:*
- 39: em_vi:*
- 40: em_ba:*
- 41: em_fun:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3230	100.0	3230	6 AR136275	AR136275 Sequence
2	3230	100.0	3230	6 E01640	E01640 gene for hu
3	3230	100.0	3230	9 HSBCEIFFI	X12706 H.sapiens g
4	3230	100.0	3230	9 HUMIL5	J03478 Human inter
5	3228.4	100.0	3230	6 E13592	E13592 gDNA encodi
6	2940	91.0	3241	9 HUMIL5A	J02971 Human eosin
7	2940	91.0	5186	9 AF353265	AF353265 Homo sapi
8	2940	91.0	57186	9 AC004042	AC004042 Homo sapi
9	2940	91.0	160042	9 AC079320	AC079320 Homo sapi
10	2940	91.0	169385	9 AC116366	AC116366 Homo sapi
11	2256.2	69.9	3507	9 HUM21DC94Z	LA8478 Homo sapien
12	1171.2	36.3	1395	6 A21910	A21910 partial gen
13	782.8	24.2	3710	9 HUM21DC93Z	LA8477 Homo sapien
14	687	21.3	700	6 AX182853	AX182853 Sequence
15	686.4	21.3	700	6 AX182850	AX182850 Sequence
16	640.4	19.8	700	6 AX182852	AX182852 Sequence
17	627.4	19.4	700	6 AX182851	AX182851 Sequence
18	626	19.4	5397	6 AX345947	AX345947 Sequence
19	622.4	19.3	700	6 AX182854	AX182854 Sequence
20	616.4	19.1	5397	6 AX345946	AX345946 Sequence
21	600.6	18.6	1658	4 AF331920	AF331920 Canis fam
22	562.8	17.4	1140	4 OALVL1	U17052 Ovis aries
23	479.4	14.8	816	6 E01639	E01639 CDNA encodi
24	479.4	14.8	816	6 E13591	E13591 CDNA encodi
25	479.4	14.8	816	9 HSLIL5R	X04688 Human mRNA
26	477.8	14.8	816	9 HSBCEFFI	X12705 H.sapiens m
27	406.8	12.6	700	6 AX182849	AX182849 Sequence
28	367	11.4	367	11 G06365	G06365 human STS w
29	360	11.1	1328	6 AB7003	AB7003 Sequence 94
30	360	11.1	1328	6 AR048415	AR048415 Sequence
31	354.4	11.0	700	6 AX182855	AX182855 Sequence
32	240.4	7.4	450	4 OALVL2	U17053 Ovis aries
33	230.4	7.1	838	4 AF025436	AF025436 Felis cat
34	198.6	6.1	1945	10 RINT5G	X54419 R.rattus ge
35	163.6	5.1	444	6 AX040771	AX040771 Sequence
36	161.8	5.0	6727	6 AR136198	AR136198 Sequence
37	161.8	5.0	6727	10 MML5G	X06271 Murine gene
38	161.8	5.0	121121	10 AL645741	AL645741 Mouse DNA
39	161.8	5.0	142732	10 AC084392	AC084392 Mus muscu
40	152.4	4.7	610	4 AF331919	AF331919 Canis fam
41	151.4	4.7	208236	2 AC073292	AC073292 Mus muscu
42	151.4	4.7	237823	2 AC020886	AC020886 Mus muscu
43	142.4	4.4	405	9 MMU19848	U19848 Macaca mula
44	136.2	4.2	405	9 CEYIN5A	L26033 Cercopithec
45	134.4	4.2	421	12 SYNIL5A	M33949 Synthetic h

ALIGNMENTS

RESULT 1
LOCUS AR136275 3230 bp DNA linear PAT 16-JUN-2001
DEFINITION Sequence 78 from patent US 6136603.
ACCESSION AR136275
VERSION AR136275.1 GI:14476947
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 3230)
AUTHORS Dean,N.M., Karras,J.G. and McKay,R.
TITLE Antisense modulation of interleukin-5 signal transduction
JOURNAL Patent: US 6136603-A 78 24-OCT-2000;
FEATURES Location/Qualifiers

source 1. .3230
/organism="unknown"
BASE COUNT 1027 a 545 c 622 g 1036 t
ORIGIN
Query Match 100.0%; Score 3230; DB 6; Length 3230;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATCCTAATCAGACCCCGACGATGAACAGAACTCGACCTGCCAAGGCTTGCCATTTCATT 60
Db 1 ATCCTAATCAGACCCCGACGATGAACAGAACTCGACCTGCCAAGGCTTGCCATTTCATT 60
QY 61 CAATCACTGCTCTCCACAGATATTTCAATTTCTTTAAGACAGATTAACTAGCCACA 120
Db 61 CAATCACTGCTCTCCACAGATATTTCAATTTCTTTAAGACAGATTAACTAGCCACA 120
QY 121 GTCATAGTAGAACATAGCCGATCTTGAAAAAACAATCCCAATATTTATGATTTAGC 180
Db 121 GTCATAGTAGAACATAGCCGATCTTGAAAAAACAATCCCAATATTTATGATTTAGC 180
QY 181 ATAAAAATCTGTTAGTGTCTACCTTATCTTTGTCACACATCTTTAAGAGAA 240
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QY 241 GTTAATTTTCTGATTTTAAAGAAATGCAATGTGGGCAATGATGATTAACCCAAAGATT 300
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Db 301 CCTTCCGTAATAGAAAAATGTTTTAAAGGGGGGAAACAGGGATTTTATTTAAAGAT 360
QY 361 AAAAGTAAATTTATTTTAAAGATATAGGCATGGAACATTTAGTTTACGATATGCC 420
Db 361 AAAAGTAAATTTATTTTAAAGATATAGGCATGGAACATTTAGTTTACGATATGCC 420
QY 421 ATTATTTAGGCATCTCTATCTGATTTAGAAATTTATCTTTCTCAAGACAGACAAT 480
Db 421 ATTATTTAGGCATCTCTATCTGATTTAGAAATTTATCTTTCTCAAGACAGACAAT 480
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QY 541 CGTTTCAGAGCCATGAGATGCTTCTGATTTGAGTTGCTAGCTCTTGAGCTGCCCTAC 600
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QY 601 GTCATAGCCATCCCGACAGAAATCCACAGTGCATTTGGTGAAGAGACCTTGGCACTG 660
Db 601 GTCATAGCCATCCCGACAGAAATCCCGACAGTGCATTTGGTGAAGAGACCTTGGCACTG 660
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Db 661 CTTTCTACTCATGCACTCTGCTGATAGCCCAATGAGTAATTTCTTTATGATTTCTTACA 720
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Db 721 GTCGTAAAGTGCATAGGTAATCATTTGTGATGTTCTTACTATATAGAGATCTGT 780
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Db 781 TATTAATATATAGATTTGAGCACATTTAGTACATGGGTGATTAATCATCACGCAAAAC 840
QY 841 ATCTGTAAAGATTAAGATGCTGCTGCTGTAATAAATGATTTGATTTCTTCTCTCT 900
Db 841 ATCTGTAAAGATTAAGATGCTGCTGCTGTAATAAATGATTTGATTTCTTCTCTCT 900
QY 901 CCAGACTCTGAGGATTCCTGCTCTGTACATAAAAATGTAAGTTAAATATGATTCAGTA 960
Db 901 CCAGACTCTGAGGATTCCTGCTCTGTACATAAAAATGTAAGTTAAATATGATTCAGTA 960

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QY 1081 AAATATGAGGAATGACTTTTATCAAGTAGAATCCTTTAAACAAGTGATTAGCTCTT 1140
Db 1081 AAATATGAGGAATGACTTTTATCAAGTAGAATCCTTTAAACAAGTGATTAGCTCTT 1140
QY 1141 GGTGATGTTGTTAGTTTGGCTTCCCAAGAGCATCGTGCAGGATTTCTTCCAGAGAT 1200
Db 1141 GGTGATGTTGTTAGTTTGGCTTCCCAAGAGCATCGTGCAGGATTTCTTCCAGAGAT 1200
QY 1201 TCCACACTGAGTGAGAGGTGCGTCTAGTCTCCGTCAGTTCTGACTCTTCTCACTTA 1260
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Db 1261 ACGTGTCTGAAAATATTAGCAACTCAGAAATTAATTTTGAACCATGATGATAGAC 1320
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QY 1381 ATATGATGCTGTATGATGATTAATGCTGCTGCTATTAATTAATTAATTAATGACT 1440
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Db 1501 TAAATGTAATGCAATTACACTTCCAAACAATTTTCCAGTTACATTAATTAAGTTAT 1560
QY 1561 CCTTATTAATACTCCTCAGTAATCATTAAGCTTCATCTTTTGAAAAATTTATCTT 1620
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QY 1621 AATATGCTGCTGTTTGTGCTTGAAGAAACAAACAACTCTTGAGAGAGGAACTCA 1680
Db 1621 AATATGCTGCTGTTTGTGCTTGAAGAAACAAACAACTCTTGAGAGAGGAACTCA 1680
QY 1681 TGTAAATACCAAAACAAAGCTTAACCTTTGTGAGACCAAAATGTTTAAATTAATTTT 1740
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Db 1861 TTTAAAAATTTTCTCATTTAGACCAACTGTGCACATGAAGAAATCTTTACAGGAATAGG 1920
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Db 1921 CACACTGAGAGTCAAACTGTGCAAGGGGGTACTGTGGAAGAACTATTCAAAACTTGTG 1980
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Db 1981 CTTAATTAAGAAATACATTTGACGGCCAAAAAGTAACTTACACATTCATGGAAGCTAT 2040
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Db	2041	ATTGTGCTGGCTGTGCTTATTTCTATGGAATGACAGTTTCTGTAAATACCTATTGTGCA	2100
QY	2101	TTTTTCTTTTTTCACAGAAAAAGTGTGAGAGAAGAACGAGAGTAACCAATTCCTAG	2160
Db	2101	TTTTTCTTTTTTCACAGAAAAAGTGTGAGAGAAGAACGAGAGTAACCAATTCCTAG	2160
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Db	2161	ACTACCTGCAAGAGTTTCTTGGTGTAAATGAACACCGAGTGGATATAGAAAGTTGAGACT	2220
QY	2221	AAACTGGTTTGTGTGACGCCCAAGATTTTGGAGGAGAAGGACATTTTACTGCAGTGAGAA	2280
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QY	2701	AAGTCTCAAGGTTGCAAGGCACACACAGAGGTGGAAGTCAATCTAGCAGACTTTAGTGGGA	2760
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QY	2761	TGTGGGAGCAGGACACAGGCGAGGAGGTGAACCTGCTTTCTCTACAGTATATCCAG	2820
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RESULT 2			
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LOCUS	E01640	3230 bp	DNA linear PAT 29-SEP-1997
DEFINITION	gene for human B cell differentiation factor.		
ACCESSION	E01640		
VERSION	E01640.1	GI:2169893	
KEYWORDS	JP 1988185387-A/2.		
SOURCE	JP 1988185387-A/2.		
ORGANISM	Homo sapiens.		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
REFERENCE	1 (bases 1 to 3230)		
AUTHORS	Honshiyu, Y., Takatsu, K. and Eba, S.		
TITLE	HUMAN B CELL DIFFERENTIATION FACTOR		
JOURNAL	Patent: JP 1988185387-A 2 30-JUL-1988;		
	HONSHIYO YU		
COMMENT	OS Human		
	PN JP 1988185387-A/2		
	PD 30-JUL-1988		
	PF 21-SEP-1987 JP 1987236842		
	PR 20-SEP-1986 JP 86P 223284		
	PI HONSHIYO YU, TAKATSU KIYOSHI, EBA SEBERINSON PC		
	C12N15/00,C07K13/00,C12N5/00,C12P21/02,(C12N5/00,C12R1:91); CC		
	strandedness: Double;		
	CC topology: Linear;		
	CC hypothetical: No;		
	CC anti-sense: No;		
	CC *source: tissue_type=fetal liver;		
	CC *source: clone=pdkCR-hIL-5gene;		
	CC Feature is identified by similarity;		
FH	Key	Location/Qualifiers	
FT	5'UTR	509..552	
FT	exon	509..696	
FT	intron	697..904	
FT	exon	905..937	
FT	intron	938..1882	
FT	exon	1883..2011	
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FT	exon	2118..2583	
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Best Local Similarity	100.0%;	Pred. No. 0;	
Matches 3230;	Conservative 0;	Mismatches 0;	Indels 0; Gaps 0;
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Db	61	CAATCACTGTCTTCCACAGATATTTTCAATTTCTTTAAGACAGATTAATCTAGCCACA	120
Qy	121	GTGATAGTAGAACATAGCCGATCTTGAAAAAACAATTCACCAATATTATGTATTTAGC	180
Db	121	GTGATAGTAGAACATAGCCGATCTTGAAAAAACAATTCACCAATATTATGTATTTAGC	180
Qy	181	ATAAAATCTGTAGTGGTCTACCTTATACCTTGTGTTTGACACACATCTTTAAGAGAA	240

Db 181 ATAAAAATCTCTTTAGTGGCTTACCTTATCTTGTGTCACACATCTTTTAAAGAGAA 240
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QY 361 AAAAGTAAATTTATTTTAAAGATATAAGGCAATGGAACATTTAGTTACAGATATGCC 420
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QY 901 CCAGACTCTGAGGATTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960
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DEFINITION X12706
ACCESSION X12706.1 GI:29392
VERSION B-cell differentiation factor.
KEYWORDS Homo sapiens.
SOURCE Homo sapiens.
ORGANISM Homo sapiens.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 3230)
AUTHORS Honjo,T., Takatu,K. and Severinson,E.
JOURNAL Unpublished
COMMENT see X12705 for ph.IL-5-30 cDNA sequence;
extent of mRNA is given according ph.IL-5-30 cDNA; Data kindly

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FEATURES
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VERSION       J03478.1 GI:186338
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ORGANISM      Homo sapiens
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TITLE         Molecular cloning and structure of the human interleukin-5 gene
JOURNAL       J. Biol. Chem. 262 (34), 16580-16584 (1987)
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AUTHORS      Tanabe,T.
TITLE         Direct Submission
JOURNAL       Submitted (09-SEP-1987) T. Tanabe, Department of Medical Chemistry,
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RESULT 5

LOCUS E13592 3230 bp DNA linear PAT 27-APR-1998
DEFINITION gDNA encoding beta-cell differentiation factor, BCDF.
ACCESSION E13592
VERSION E13592.1 GI:3252397
KEYWORDS JP 1997215496-A/2.
SOURCE Homo sapiens.
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 3230)
HONSHIYO YU, Takatsu, K. and Eba, S.
PRODUCTION OF HUMAN B CELL DIFFERENTIATION FACTOR
Patent: JP 1997215496-A 2 19-AUG-1997;
HONSHIYO YU

COMMENT

OS Homo sapiens (human)
PN JP 1997215496-A/2
PD 19-AUG-1997
PE 21-SEP-1987 JP 1996206192
PR 20-SEP-1986 JP 86P 223284
PI HONSHIYO YU, TAKATSU KIYOSHI, EBA SEBERINSON PC
C12N15/09, A61K38/00, A61K38/00, C07H21/04, C07K14/47, PC
C12N5/10,
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/db_xref='taxon:9606'
BASE COUNT 1027 a 544 c 623 g 1036 t
ORIGIN

Query Match 100.0%; Score 3228.4; DB 6; Length 3230;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3229; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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RESULT 6

HUMIL5A

LOCUS 3241 bp DNA linear PRI 29-APR-1996

DEFINITION Human eosinophil differentiation factor (interleukin 5) gene,
complete cds.

ACCESSION J02971 GI:186340

VERSION J02971.1

KEYWORDS eosinophil differentiation factor; interleukin 5.

SOURCE Homo sapiens (clone: beta-EDFH-1.) (clone library: lambda-EDFH-1)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 3241)

AUTHORS Campbell,H.D., Tucker,W.Q., Hort,Y., Martinson,M.E., Mayo,G.,
Clutterbuck,E.J., Sanderson,C.J. and Young,I.G.TITLE Molecular cloning, nucleotide sequence, and expression of the gene
encoding human eosinophil differentiation factor (interleukin 5)

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 84 (19), 6629-6633 (1987)

MEDLINE 88016145

PUBMED 3498940

COMMENT Draft entry and computer-readable sequence for [1] kindly provided
by H.D.Campbell, 09-SEP-1987.

FEATURES Location/Qualifiers

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DEFINITION Homo sapiens chromosome 5, clone RP11-729C24, complete sequence.

ACCESSION AC079320

VERSION AC079320.9 GI:21747557

KEYWORDS HTG.

SOURCE human.

ORGANISM Homo sapiens

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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS Birren,B., Nusbaum,C. and Lander,E.

TITLE Homo sapiens chromosome 5, clone RP11-729C24

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 160042)
Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,

TITLE	Direct Submission
JOURNAL	Submitted (27-AUG-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
REFERENCE	3 (bases 1 to 160042)
AUTHORS	Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S., Barna,N., Bastien,V., Boguslavskiy,L., Boukhgalter,B., Brown,A., Camarata,J., Campopiano,A., Chang,J., Chazaro,B., Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cooke,P., Cooke,P., Dearellano,K., Dewar,K., Diaz,J.S., Dodge,S., Ferreira,P., Ferreira,P., Fitzhugh,W., Gage,D., Galagan,J., Gardyna,S., Ginde,S., Goyette,M., Hagos,B., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C., Kamat,A., Karatas,A., Kells,C., LaRocque,K., Lamazares,R., Landers,T., Lehoczký,J., Levine,R., Liu,G., Maclean,C., Macdonald,P., Major,J., Marquis,N., Matthews,C., McCarthy,M., McEwan,P., McKernan,K., Meldrim,J., Menus,L., Mihova,T., Mlenga,V., Murphy,T., Naylor,J., Nguyen,C., Nicol,R., Norbu,C., Norman,C.H., O'Connell,T., O'Donnell,P., O'Neill,D., Oliver,J., Peterson,K., Phunkhang,P., Piere,N., Pollara,V., Raymond,C., Relta,R., Rieback,M., Riley,R., Rise,C., Rogov,P., Roman,J., Rosetti,M., Roy,A., Santos,R., Schauer,S., Schuback,R., Seaman,S., Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N., Straus,N., Subramanian,A., Talamas,J., Testaye,S., Theodore,J., Topham,K., Travers,M., Travis,N., Triggillo,J., Vassiliev,H., Viel,R., Vo,A., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G., Zainoun,J., Zimmer,A., and Zody,M.
TITLE	Direct Submission
JOURNAL	Submitted (16-FEB-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
REFERENCE	4 (bases 1 to 160042)
AUTHORS	Birren,B., Nusbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S., Barna,N., Bastien,V., Bloom,T., Boguslavskiy,L., Boukhgalter,B., Camarata,J., Chang,J., Chazaro,B., Choepel,Y., Collymore,A., Cooke,P., Cooke,P., Dearellano,K., Dewar,K., Diaz,J.S., Dodge,S., Ferreira,P., Fitzhugh,W., Gage,D., Galagan,J., Gardyna,S., Ginde,S., Goyette,M., Iliev,I., Johnson,R., Jones,C., Kamat,A., Karatas,A., Kells,C., LaRocque,K., Lamazares,R., Landers,T., Lehoczký,J., Levine,R., Liu,G., Maclean,C., Macdonald,P., Major,J., Marquis,N., Matthews,C., McCarthy,M., McEwan,P., McKernan,K., Meldrim,J., Menus,L., Mihova,T., Mlenga,V., Murphy,T., Naylor,J., Nguyen,C., Nicol,R., Norbu,C., Norman,C.H., O'Connell,T., O'Donnell,P., O'Neill,D., Oliver,J., Peterson,K., Phunkhang,P., Piere,N., Pollara,V., Raymond,C., Relta,R., Rieback,M., Riley,R., Rise,C., Rogov,P., Roman,J., Rosetti,M., Roy,A., Santos,R., Schauer,S., Schuback,R., Seaman,S., Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N., Straus,N., Subramanian,A., Talamas,J., Testaye,S., Theodore,J., Topham,K., Travers,M., Travis,N., Triggillo,J., Vassiliev,H., Viel,R., Vo,A., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G., Zainoun,J., Zembek,L., Zimmer,A., and Zody,M.

Faro, S., Ferreira, P., Fitzgerald, M., Gage, D., Galagan, J., Gardyna, S., Gord, S., Graham, L., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kanat, A., Karatas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, G., Maclean, C., Macdonald, P., Major, J., Matthews, C., McCarthy, M., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunhkhang, P., Pierre, N., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Roy, A., Schauer, S., Schuback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wymann, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

Direct Submission
Submitted (14-JUL-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
On Jul 14, 2002 this sequence version replaced gi:18677463.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: <http://www-seq.wi.mit.edu>
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: L10831
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Query Match 91.0%; Score 2940; DB 9; Length 160042;
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Db 90085 ACGTTTCAGAGCCATGAGATGCTTCTGCAATTTGAGTTTGTAGCTCTTGGAGCTGCCA 90026
QY 600 CGTGATGCCATCCCCACAGAAATTTCCACAAAGTGCATTTGGTGAAGAGACCTGGCACT 659
Db 90025 CGTGATGCCATCCCCACAGAAATTTCCACAAAGTGCATTTGGTGAAGAGACCTGGCACT 89966
QY 660 GCTTCTACTCATGCACTCTGCTGATAGCCAAAGTAATTTCTTTATGATTTCTCTAC 719
Db 89965 GCTTCTACTCATGCACTCTGCTGATAGCCAAAGTAATTTCTTTATGATTTCTCTAC 89906
QY 720 AGTCTGTAAGTGCATGAGTAATCATTTGTGATGCTTCTTACTATATATAGATCTG 779
Db 89905 AGTCTGTAAGTGCATGAGTAATCATTTGTGATGCTTCTTACTATATATAGATCTG 89846
QY 780 TTATAAATTAATAGATTTGAGCACATTTAGTACATGGGTGATTAACATACACACACAAA 839
Db 89845 TTATAAATTAATAGATTTGAGCACATTTAGTACATGGGTGATTAACATACACACACAAA 89786
QY 840 CATCTCTGTTAAAGTATGATGCTGTGTGCTGTAATAATGATTTCTTTCTCTC 899
Db 89785 CATCTCTGTTAAAGTATGATGCTGTGTGCTGTAATAATGATTTCTTTCTCTC 89726
QY 900 TCCAGACTCTGAGGATTCCTGTTCTCTGATACATAAAAATGTAAGTTAAATTAATGATTCAGT 959
Db 89725 TCCAGACTCTGAGGATTCCTGTTCTCTGATACATAAAAATGTAAGTTAAATTAATGATTCAGT 89666
QY 960 AAAATGATGGCATGAATAGTAATTTCTCTGTTTAAAGCTGTAATCATTAATGATTCAT 1019
Db 89665 AAAATGATGGCATGAATAGTAATTTCTCTGTTTAAAGCTGTAATCATTAATGATTCAT 89606
QY 1020 GGAATCTATTTAATTTCTATAATTTGTTTTCATATGGGTGGCTGTAATGCTGTACTTA 1079
Db 89605 GGAATCTATTTAATTTCTATAATTTGTTTTCATATGGGTGGCTGTAATGCTGTACTTA 89546
QY 1080 TAAATATGAGGAATGACTTTTATCAAGTAGAAATCCTTTAAACAAGTGAATGAGCTCTT 1139
Db 89545 TAAATATGAGGAATGACTTTTATCAAGTAGAAATCCTTTAAACAAGTGAATGAGCTCTT 89486
QY 1140 TGGTGAATGTTGTTAGTTCCTTCCCAAGAGACATGCTGCA--GGATTTTTCAGAGAG 1198
Db 89485 TGGTGAATGTTGTTAGTTCCTTCCCAAGAGACATGCTGCA--GGATTTTTCAGAGAG 89427
QY 1199 ATTCACACTGAGTGAAGGTGCGTGTAGTTCGCTGACAGTTCTGACTCTTTCTCACTC 1258
TT

Db 89426 ATTCACACTGAGTGAAGGTGCGTGTAGTTCGCTGACAGTTCTGACTCTTTCTCACTC 89367
QY 1259 TAACGTGTTCTGAAAGTATTAGCAACTCAGAAATTTATTTTGAACCATGATCAGTAG 1318
Db 89366 TAACGTGTTCTGAAAGTATTAGCAACTCAGAAATTTATTTTGAACCATGATCAGTAG 89307
QY 1319 ACATTAATAATATATACAAATGCCCTATATTTAATA--TTCGTCACTACTTAATAATATATG 1377
Db 89306 ACATTAATAATATATACAAATGCCCTATATTTAATAATTTCTGCACTACTTAATAATATATG 89247
QY 1378 ACTATATGATGGTG--TGTATGCAAT--GAATATGCCGTGTCATATTTAAATGTAAATAT 1434
Db 89246 ACTATATGATGGTGTTGTATGCAATTTGAATATGTCTGTCATATTTAAATGTAAATAT 89187
QY 1435 ATAG--TTTATTAGTCTAAATAGAAATAAACTACAGCTAGAACTGTAGAAACACATTTGAT 1493
Db 89186 ATAGTTTATTAATAGTCTAAATAGAAATAAACTACAGCTAGAACTGTAGAAACACATTTGAT 89127
QY 1494 ATGATTTAATGTATTAATGCAATTCACCTTCCAAACATTTTTCAGTTACATTAATTA 1553
Db 89126 ATGATTTAATGTATTAATGCAATTCACCTTCCAAACATTTTTCAGTTACATTAATTA 89067
QY 1554 GTTATATCCTTTATAAAACCTCCAGTAATCATATTAAGCTTCATCTACTTTTGAATAAT 1613
Db 89066 GTTATATCCTTTATAAAACCTCCAGTAATCATATTAAGCTTCATCTACTTTTGAATAAT 89007
QY 1614 TTATCTTAATATGT 1673
Db 89006 TTATCTTAATATGT 88947
QY 1674 GAACATGATTAATACACAAACAAAGCCTTAACCTTTGTGACCCAAATTTGTTTAATA 1733
Db 88946 GAACATGATTAATACACAAACAAAGCCTTAACCTTTGTGACCCAAATTTGTTTAATA 88887
QY 1734 TTATTTTAAATTTGATGAATTTAAAGTATATATATTTATTTGTGTACAAATATGATGTTT 1793
Db 88886 TTATTTTAAATTTGATGAATTTAAAGTATATATATTTATTTGTGTACAAATATGATGTTT 88827
QY 1794 GAAGTATGATTAATTTGACAGAAATGACAAATGACCAAAATTTTATACCTGTGTGATTA 1853
Db 88826 GAAGTATGATTAATTTGACAGAAATGACAAATGACCAAAATTTTATACCTGTGTGATTA 88767
QY 1854 TTTGCATTTTAAAAATTTTCTCATTTTAGCACCAACTGTGCACTGAAGAAATCTTTCAGG 1913
Db 88766 TTTGCATTTTAAAAATTTTCTCATTTTAGCACCAACTGTGCACTGAAGAAATCTTTCAGG 88707
QY 1914 GAATAGCACACTGAGAGTCAAACTGTGCAAGGGGGTACTGTGAAAGACATTTCAAAA 1973
Db 88706 GAATAGCACACTGAGAGTCAAACTGTGCAAGGGGGTACTGTGAAAGACATTTCAAAA 88647
QY 1974 ACTGTCCCTAATAAAGAAATATGACGCGCCAAAAAGTAAGTTACACACATTCATG 2033
Db 88646 ACTGTCCCTAATAAAGAAATATGACGCGCCAAAAAGTAAGTTACACACATTCATG 88587
QY 2034 AAGCTATATTTGCTGCTGCTGCTATTTCTATGGAATGACAGTTTCTGTATACT 2093
Db 88586 AAGCTATATTTGCTGCTGCTGCTATTTCTATGGAATGACAGTTTCTGTATACT 88528
QY 2094 ATTGTCAATTTTCTTTTTCACAGAAAAAGTGTGAGAGAAAGACGAGAGATTAACCA 2153
Db 88527 ATTGTCAATTTTCTTTTTCACAGAAAAAGTGTGAGAGAAAGACGAGAGATTAACCA 88468
QY 2154 TTCCATAGACTACCTGCAAGAGTTTCTGTGTAAATGAACACCGAGTGAATTAAGAAAGT 2213
Db 88467 TTCCATAGACTACCTGCAAGAGTTTCTGTGTAAATGAACACCGAGTGAATTAAGAAAGT 88408
QY 2214 TGAGACTAACTGTTTGTGAGCCAAAGATTTTGAGAGAGAGACATTTTACTGCAG 2273
Db 88407 TGAGACTAACTGTTTGTGAGCCAAAGATTTTGAGAGAGAGACATTTTACTGCAG 88348
QY 2274 TGAGAAATGAGGCGCAAGAAAGTCAAGCCTTAATTTCAATATTAATTTAATTCAGAGG 2333
Db 88347 TGAGAAATGAGGCGCAAGAAAGTCAAGCCTTAATTTCAATATTAATTTAATTCAGAGG 88288

QY	2334	GAAGTAATATTTTCAGGCATACAGCACTTTGCCAGAAAGCATAAATTCCTTAAATAT	2393
Db	88287	GAAGTAATATTTTCAGGCATACAGCACTTTGCCAGAAAGCATAAATTCCTTAAATAT	88228
QY	2394	ATTTCAGATATCAGAATCATTTGAAGTATTTTCTCCAGGCCAAAATGATATACCTTTTTC	2453
Db	88227	ATTTCAGATATCAGAATCATTTGAAGTATTTTCTCCAGGCCAAAATGATATACCTTTTTC	88168
QY	2454	TTATTTAACTTAAACATTTCTGTAATAATGCTGTAACTTAATAGTATTTATGAATGGTTA	2513
Db	88167	TTATTTAACTTAAACATTTCTGTAATAATGCTGTAACTTAATAGTATTTATGAATGGTTA	88108
QY	2514	AGATTTTGGTAAATTAGTATTTATTTAATGTTATGTTGTGTTCTAATAAACAAAATAG	2573
Db	88107	AGATTTTGGTAAATTAGTATTTATTTAATGTTATGTTGTGTTCTAATAAACAAAATAG	88048
QY	2574	ACAACGTTCATTTTGTGCTGCGCTCTGTCTTAGCAATTTGAACTTAGCACAGTCCAT	2633
Db	88047	ACAACGTTCATTTTGTGCTGCGCTCTGTCTTAGCAATTTGAACTTAGCACAGTCCAT	87990
QY	2634	TGAGTACATGCCCCAGTTTGGAGGAGGGTCTGAGCACATGTGGCTGAGCATCCCATTTTC	2693
Db	87989	TGAGTACATGCCCCAGTTTGGAGGAGGGTCTGAGCACATGTGGCTGAGCATCCCATTTTC	87930
QY	2694	TCTGGAGAAAGTCTCAAGGTTGCAAGGCACACACAGAGGTGAAGTGATCTAGCAGACTTA	2753
Db	87929	TCTGGAGAAAGTCTCAAGGTTGCAAGGCACACACAGAGGTGAAGTGATCTAGCAGACTTA	87870
QY	2754	GTTGGGATGTGGGAGCAGGACAGGACAGGAGGTGAACCTGGTTTCTCTCTACAGTA	2813
Db	87869	GTTGGGATGTGGGAGCAGGACAGGACAGGAGGTGAACCTGGTTTCTCTCTACAGTA	87810
QY	2814	TATCCAGAACCTGGATGGTGCAGGGGTAAATGTTAGGGAATTAATGAATGAATGTCGTT	2873
Db	87809	TATCCAGAACCTGGATGGTGCAGGGGTAAATGTTAGGGAATTAATGAATGAATGTCGTT	87751
QY	2874	TCCAAGA-TGATTTAGAACCTAAATGAGTTGTAAG--CTCCCCTGGAAGAAAGGATGT-	2929
Db	87750	TCCAAGACTGATTTGTAAGACTTAATGAGTTGTAAGGCGTCCCTGGGAAGAAAGGAGTG	87691
QY	2930	--GGAACCTGTAACCTAGGTTCTGCCCCAGCCTGTGAGAAGAAATTTGGCAGATC-ATCTCA	2986
Db	87690	TGGGAACCTGTAACCTAGGTTCTGCCCCAGCCTGTGAGAAGAAATTTGGCAGATCAATCTCA	87631
QY	2987	TTCAGATATAGAGAGGAAGCCAGAAACCCTCTCTGCCAAGGCTTCAGAGGGTCTTA--	3044
Db	87630	TTCAGATATAGAGAGGAAGCCAGAAACCCTCTCTGCCAAGGCTTCAGAGGGTCTTAAC	87571
QY	3045	CCACCTGACCCCTGCACCATTAACAAGG-ACAGAGAGACA-TGGTAGGGCAGTCCCATTTA	3102
Db	87570	CCACCTGACCCCTGCACCATTAACAAGG-ACAGAGAGACA-TGGTAGGGCAGTCCCATTTA	87511
QY	3103	GAAAGACTGAGTTCCGTATTTCC--GGGGCAGGGCAGCAGCAGGCCGACACAACA-TCCATT	3160
Db	87510	GAAAGACTGAGTTCCGTATTTCC--GGGGCAGGGCAGCAGCAGGCCGACACAACA-TCCATT	87451
QY	3161	CTGCCCTGCTTATGGCTATCAGTAGCATCCTAGAGATTCTCTGTTTGAGAAAACCTTCTC	3220
Db	87450	CTGCCCTGCTTATGGCTATCAGTAGCATCCTAGAGATTCTCTGTTTGAGAAAACCTTCTC	87391

RESULT 10				
AC116366/c				
LOCUS	AC116366	169385 bp	DNA	linear
DEFINITION	Homo sapiens chromosome 5 clone RP11-89G4,			PRI 22-MAY-2002
ACCESSION	AC116366			complete sequence.
VERSION	AC116366.2	GI:21070669		
KEYWORDS	HTG.			
SOURCE	Homo sapiens.			
ORGANISM	Homo sapiens			
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			

REFERENCE	1 (bases 1 to 169385)	DOE Joint Genome Institute and Stanford Human Genome Center.
AUTHORS	Direct Submission	
TITLE	Unpublished	
JOURNAL	2 (bases 1 to 169385)	
REFERENCE	DOE Joint Genome Institute.	
AUTHORS	Direct Submission	
TITLE	Submitted (27-MAR-2002) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA	
JOURNAL	3 (bases 1 to 169385)	
REFERENCE	DOE Joint Genome Institute and Stanford Human Genome Center.	
AUTHORS	Direct Submission	
TITLE	Submitted (22-MAY-2002) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA	
JOURNAL	On May 22, 2002 this sequence version replaced gi:19745048.	
COMMENT	Draft Sequence Produced by DOE Joint Genome Institute www.jgi.doe.gov	
FEATURES	Finishing Completed at Stanford Human Genome Center www.shgc.stanford.edu Quality: Phrap Quality >=40 99.9% of Sequence; Estimated Total Number of Errors is 0.1. Location/Qualifiers 1. 169385 /organism="Homo sapiens" /db_xref="taxon:9606" /chromosome="5" /clone="RP11-89G4"	
BASE COUNT	46926 a 39090 c 38418 g 44951 t	
ORIGIN		
Query Match	91.0%; Score 2940; DB 9; Length 169385;	
Best Local Similarity	98.5%; Pred. No. 0;	
Matches 3191; Conservative	0; Mismatches 20; Indels 29; Gaps 2	
QY 1	ATCCTAATCAAGACCCAGTGAACAGAACTCGACCCCTGCCAAGGCTTGCA-TTTCATT	59
Db 155584	ATCCTAATCAAGACCCAGTGAACAGAACTCGACCCCTGCCAAGGCTTGCAATT	155525
QY 60	TCAATCACTGCTCTCCACCAAGTATTTTCAATTCTTTAAGACAGATTAACTAGCCAC	119
Db 155524	TCAATCACTGCTCTCCACCAAGTATTTTCAATTCTTTAAGACAGATTAACTAGCCAC	155465
QY 120	AGTCATAGTAGAACATAGCCGATCTTGAAAAAACAATCCCAATATTATGTATTTAG	179
Db 155464	AGTCATAGTAGAACATAGCCGATCT--GAAAAAACAATCCCAATATTATGTATTTAG	155407
QY 180	CATAAAATTCTGTTAGTGGTCTACCTTATCTTGTGTTGCACACATCTTTAAGAGGA	239
Db 155406	CATAAAATTCTGTTAGTGGTCTACCTTATCTTGTGTTGCACACATCTTTAAGAGGA	155347
QY 240	AGTTAATTTTCTGATTTTAAAGAAATGCAAAATGTGGGGCAATGATTTAACCCAAAGAT	299
Db 155346	AGTTAATTTTCTGATTTTAAAGAAATGCAAAATGTGGGGCAATGATTTAACCCAAAGAT	155287
QY 300	TCCTTCCGTAATAGAAATGTTTTTAAAGGGGGGAAACAGGGATTTTATTATTAAGA	359
Db 155286	TC--TTCGTAATAGAAATGTTTTTAAAGGGGGGAAACAGGGATTTTATTATTAAGA	155229
QY 360	TAAAGTAAATTTATTTTAAAGATATTAAGGCATGGAACATTTAGTTTCACGATATGC	419
Db 155228	TAAAGTAAATTTATTTTAAAGATATTAAGGCATGGAACATTTAGTTTCACGATATGC	155169
QY 420	CATTATTAGGCATCTCTATCTGATTGTTAGAAATTAATCTTCCCTCAAGACAGACAA	479
Db 155168	CATTATTAGGCATCTCTATCTGATTGTTAGAAATTAATCTTCCCTCAAGACAGACAA	155109
QY 480	TAAATTGACTGGGAGCAGTCTTGACTATGACATTTCTTGCCAAAGGCAACGACGA	539
Db 155108	TAAATTGACTGGGAGCAGTCTTGACTATGACATTTCTTGCCAAAGGCAACGACGA	155049
QY 540	ACGTTTCAGAGCCATGAGATGCTTCTGCATTTGAGTTTGCTAGCTCTGGAGCTGCCTA	599
Db 155048	ACGTTTCAGAGCCATGAGATGCTTCTGCATTTGAGTTTGCTAGCTCTTGAGAGCTGCCTA	154989

QY	600	CGTGTATGCCATCCCCACAGAAATTTCCCAACAGTGCATTTGGTGAAGAAGACCCTTGGCACT	659
Db	154988	CGGTATAGCCATCCCCACAGAAATTTCCCAACAGTGCATTTGGTGAAGAAGACCCTTGGCACT	154929
QY	660	GCTTTCTACTCATCGAACTCTGCTGATAGCCAAATGAGGTAATTTCTTATGATTCCTAC	719
Db	154928	GCTTTCTACTCATCGAACTCTGCTGATAGCCAAATGAGGTAATTTCTTATGATTCCTAC	154869
QY	720	AGTCTGTAAGTGCATAGGTAATCATTTTGTGATGGTTCCCTTACTATATATAGAGATCTG	779
Db	154868	AGTCTGTAAGTGCATAGGTAATCATTTTGTGATGGTTCCCTTACTATATATAGAGATCTG	154809
QY	780	TTATTAATTAATTAAGATTCTGAGCACATTAGTACATGGGTGATACTACATCCACAGCAA	839
Db	154808	TTATTAATTAATTAAGATTCTGAGCACATTAGTACATGGGTGATACTACATCCACAGCAA	154749
QY	840	CATTCTGTTAAAAGTTATGAATGCTGGTGTGCTGTAAAATGATTTGTATTTCCCTTCCCTC	899
Db	154748	CATTCTGTTAAAAGTTATGAATGCTGGTGTGCTGTAAAATGATTTGTATTTCCCTTCCCTC	154689
QY	900	TCCAGACTCTGAGGATTCCTGTTCCCTGTACATAAAATGTAAGTTAAATTTATGATTCAGT	959
Db	154688	TCCAGACTCTGAGGATTCCTGTTCCCTGTACATAAAATGTAAGTTAAATTTATGATTCAGT	154629
QY	960	AAATGATGGCATGAATTAAGTAATTTCCCTGTTTAAAGCTGTAATCATTTAGTTATCATTT	1019
Db	154628	AAATGATGGCATGAATTAAGTAATTTCCCTGTTTAAAGCTGTAATCATTTAGTTATCATTT	154569
QY	1020	GGAACATATTTAATTTTCTAATATTTTGTTTTCATATAGGCTGGCTGTGAATGCTGTACTTA	1079
Db	154568	GGAACATATTTAATTTTCTAATATTTTGTTTTCATATAGGCTGGCTGTGAATGCTGTACTTA	154509
QY	1080	TAAATATGAGGAATGACTTTTATCAAGTAGAATTCCTTAAACAAGTGATTTAGGCTCTT	1139
Db	154508	TAAATATGAGGAATGACTTTTATCAAGTAGAATTCCTTAAACAAGTGATTTAGGCTCTT	154449
QY	1140	TGGTGATGTTGTTAGTTTGGCTTCCCAAAAGACATCGTGTCA - GGATTCTTCCAGAAAG	1198
Db	154448	TGGTGATGTTGTTAGTTTGGCTTCCCAAAAGACATCGTGTGTCAAGGATTTCTTCCAGAAAG	154390
QY	1199	ATTCCACACTGAGTGAGAGGTGCGTGTAGTCTCCGTGCAGTTCTGACTCTTCTCACTC	1258
Db	154389	ATTCCACACTGAGTGAGAGGTGCGTGTAGTCTCCGTGCAGTTCTGACTCTTCTCACTC	154330
QY	1259	TAAAGTGTTCCTGAAGATATTAGCAACTCAGAAATTATTTTGAACCATGATCAGTAG	1318
Db	154329	TAAAGTGTTCCTGAAGATATTAGCAACTCAGAAATTATTTTGAACCATGATCAGTAG	154270
QY	1319	ACATTTAAAATATATTAACAAGTCCCTATATTTAATTA - TTCTGCATACTTAAATATTTATG	1377
Db	154269	ACATTTAAAATATATTAACAAGTCCCTATATTTAATTAATTTCTGCATACTTAAATATTTATG	154210
QY	1378	ACTATATGATGGTG - TGTATGCAATT - GAATATGCCCTGGTGCATATTTAAATGTAAAATAT	1434
Db	154209	ACTATATGATGGTGTTGTATGCAATTTGAATATGTCCCTGGTGCATATTTAAATGTAAAATAT	154150
QY	1435	ATAG - TTTATTTAGTCTAAATAGAATTAACACTACCAGAGCTAGAACTGTAGAAACACATTCAT	1493
Db	154149	ATAGTTTATTTAGTCTAAATAGAATTAACAACTACCAGAGCTAGAACTGTAGAAACACATTCAT	154090
QY	1494	ATGAGTTTAAATGTATAATGCAATTACACTTCCAAAACATTTTTCAGTTACATAAATTA	1553
Db	154089	ATGAGTTTAAATGTATAATGCAATTACACTTCCAAAACATTTTTCAGTTACATAAATTA	154030
QY	1554	GTTATATTCCTTTATAAAACPCTCAGTAATCATATATAAGTTCATCTACTTTTGAAAATTT	1613
Db	154029	GTTATATTCCTTTATAAAACPCTCAGTAATCATATATAAGTTCATCTACTTTTGAAAATTT	153970
QY	1614	TTATCTTAAATATGTGGTGGTTTGTGCTTAGAAAACAACAACAACTCTTTGGAGAAG	1673
Db	153969	TTATCTTAAATATGTGGTGGTTTGTGCTTAGAAAACAACAACAACTCTTTGGAGAAG	153910

QY	1674	GAAGTATGTATACATTCGACAAATGACAATGACCAAAATTTTATACCTTGTCTGTACATATGATGTTTT	1733
Db	153909	GAAGTATGTATACATTCGACAAATGACAATGACCAAAATTTTATACCTTGTCTGTACATATGATGTTTT	153850
QY	1734	TTATTTTAAATGATGAATTAAGTATATATATTTATTTGTGTACATATGATGTTTT	1793
Db	153849	TTATTTTAAATGATGAATTAAGTATATATATTTATTTGTGTACATATGATGTTTT	153790
QY	1794	GAAGTATGTATACATTCGACAAATGACAATGACCAAAATTTTATACCTTGTCTGTACATATGATGTTTT	1853
Db	153789	GAAGTATGTATACATTCGACAAATGACAATGACCAAAATTTTATACCTTGTCTGTACATATGATGTTTT	153730
QY	1854	TTTGCATTTTAAAAATTTTCTCATTTTAGCACCAACTGTGCACCTGGAAGAAATCTTTCAGG	1913
Db	153729	TTTGCATTTTAAAAATTTTCTCATTTTAGCACCAACTGTGCACCTGGAAGAAATCTTTCAGG	153670
QY	1914	GAATAGGCACACTGGAGAGTCAAACTGTGCAAGGGGTACTGTGGAAGAGCTATTTCAAA	1973
Db	153669	GAATAGGCACACTGGAGAGTCAAACTGTGCAAGGGGTACTGTGGAAGAGCTATTTCAAA	153610
QY	1974	ACTTGTCCCTTAATAAAGAAATACATTGACGGGCCAAAAAGTAACTTACACACATTCATGG	2033
Db	153609	ACTTGTCCCTTAATAAAGAAATACATTGACGGGCCAAAAAGTAACTTACACACATTCATGG	153550
QY	2034	AAGCTATATTTGTCTGCTGCTGTGCTATTTCTATGAAATGACAGTTTCTCTGTAATACCT	2093
Db	153549	AAGCTATATTTGT - CTGGCTGTGCTATTTCTATGAAATGACAGTTTCTCTGTAATACCT	153491
QY	2094	ATTGTCATTTTCTTTTTCACAGAAAAAGTGTGAGAGAAAGACGAGAGTAACCAA	2153
Db	153490	ATTGTCATTTTCTTTTTCACAGAAAAAGTGTGAGAGAAAGACGAGAGTAACCAA	153431
QY	2154	TTCTTAGACTACCTGCAAGAGTTTCTTGCTGTAATGAACCCGAGTGATATAGAAGT	2213
Db	153430	TTCTTAGACTACCTGCAAGAGTTTCTTGCTGTAATGAACCCGAGTGATATAGAAGT	153371
QY	2214	TGAGACTAAACTGGTTTGTTCGACCCAAAGATTTTGGAGAGAGGACATTTACTGCAG	2273
Db	153370	TGAGACTAAACTGGTTTGTTCGACCCAAAGATTTTGGAGAGAGGACATTTACTGCAG	153311
QY	2274	TGAGAAATGAGGGCCAAAGAAAGTCAAGCCCTTAATTTTCAATATAATTAACCTTCAGAG	2333
Db	153310	TGAGAAATGAGGGCCAAAGAAAGTCAAGCCCTTAATTTTCAATATAATTAACCTTCAGAG	153251
QY	2334	GAAAGTAAATATTTTCAGGCATCTGACACTTTTCCAGAGCAATAAATCTTAAATAT	2393
Db	153250	GAAAGTAAATATTTTCAGGCATCTGACACTTTTCCAGAGCAATAAATCTTAAATAT	153191
QY	2394	ATTTCAGATATCAGAAATCATTTGAAGTATTTTCTCCAGGCAAAATTTGATATACTTTTTC	2453
Db	153190	ATTTCAGATATCAGAAATCATTTGAAGTATTTTCTCCAGGCAAAATTTGATATACTTTTTC	153131
QY	2454	TTATTTTAACCTTAACATTTCTGTAAATATGTCGTTAACTTAATAGTATTTATGAATGGTTA	2513
Db	153130	TTATTTTAACCTTAACATTTCTGTAAATATGTCGTTAACTTAATAGTATTTATGAATGGTTA	153071
QY	2514	AGAAATTTGGTAAATTAGTATTTAATTTAATGTTATGTTGTCTTAATAAACAAAAATAG	2573
Db	153070	AGAAATTTGGTAAATTAGTATTTAATTTAATGTTATGTTGTCTTAATAAACAAAAATAG	153011
QY	2574	ACAACTGTCAATTTGCTGCTGCTCTGTCTTAGCAATTTGAAGTTAGCACAGTTCAT	2633
Db	153010	ACAACTGTCAATTTGCTGCTGCTCTGTCTTAGCAATTTGAAGTTAGCACAGTTCAT	152953
QY	2634	TGAGTACATGCCAGTTTGGAGAAAGGCTCTGAGCACATGTGCTGAGCATCCCAATTC	2693
Db	152952	TGAGTACATGCCAGTTTGGAGAAAGGCTCTGAGCACATGTGCTGAGCATCCCAATTC	152893
QY	2694	TCTGGAGAAGTCTCAAGGTTGCAAGGCACACACAGAGGTGAAGTGAATCTAGCAGACTTA	2753
Db	152892	TCTGGAGAAGTCTCAAGGTTGCAAGGCACACACAGAGGTGAAGTGAATCTAGCAGACTTA	152833
QY	2754	GTTGGGATGTGGGAGCAGGACACAGGCAGGAGGTGAACCTGTCTTCTCTACAGTA	2813

|||||
Db 152832 GTGGGATGTGGGAGCAGGACACAGGAGGTGAACCTGGTTTCTCTACAGTA 152773
QY 2814 TATCCAGAACCTGGGATGTCGGAAGGGTAATGCTAGGAATAAATGAATGTCGTT 2873
Db 152772 TATCCAGAACCTGGGATGTT-GCAGGGTAATGCTAGGAATAAATGAATGTCGTT 152714
QY 2874 TCCAGA-TGATGTAGAACTAAATGAGTTGTAAG--CTCCCTGGAAGAAGGATGT- 2929
Db 152713 TCCAGACTGATTTGTAGAACTAAATGAGTTGTAAGGCTCCCTGGAAGAAGGAGCTG 152654
QY 2930 --GGAACCTGTAACTAGTTCCTGCCAGCCTGTGAGAAGATTTGGCAGATC-ATCTCA 2986
Db 152653 TGGGAACCTGTAACTAGTTCCTGCCAGCCTGTGAGAAGATTTGGCAGATCATTCA 152594
QY 2987 TTGCCAGTATAGAGAGAGAGAGCCAGAACCTCTCTGCAAGCCCTGCAAGGGGTCTTA-- 3044
Db 152593 TTGCCAGTATAGAGAGAGAGAGCCAGAACCTCTCTGCAAGCCCTGCAAGGGGTCTTACC 152534
QY 3045 CCACCTGACCTGCACACCATACAAAAGG-ACAGAGAGACA-TGCTAGGGCGAGTCCCATTA 3102
Db 152533 CCACCTGACCTGCACACCATACAAAAGGAGACAGACACTGGTAGGGCGAGTCCCATTA 152474
QY 3103 GAAAGACTGAGTTCCTGATTTCCC-GGGGCAAGGGCAGCAGCCAGCCGACACACA-TCCATT 3160
Db 152473 GAAAGACTGAGTTCCTGATTTCCC-GGGGCAAGGGCAGCAGCCAGCCGACACACTCCATT 152414
QY 3161 CTGCCCTGCTTATGGCTATCAGTAGACATCAGAGATTTCTGTTGAGAAAACCTCTC 3220
Db 152413 CTGCCCTGCTTATGGCTATCAGTAGACATCAGAGATTTCTGTTGAGAAAACCTCTC 152354

RESULT 11
HUM21DC94Z 3507 bp DNA linear PRI 22-OCT-1995
LOCUS HUM21DC94Z 3507 bp DNA linear PRI 22-OCT-1995
DEFINITION Homo sapiens (subclone 6_e5 from P1 H21) DNA sequence.
ACCESSION L48478
VERSION L48478.1 GI:1032381
KEYWORDS interleukin gene cluster.
SOURCE Homo sapiens (tissue library: Subclones in POT2 from P1 clone H21)
DNA.

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 3507)
AUTHORS Martin,C.H., Bondoc,M.M., Chiang,A., Cloutier,T., Davis,C.A.,
Ericsson,C.L., Jaklevic,M.A., Kim,R.J., Lee,M.T., Li,M.,
Mayeda,C.A., Stelert-El Kheir,A. and Palazzolo,M.J.
TITLE Sequencing of the Interleukin gene cluster of homo sapiens
JOURNAL Unpublished (1995)
COMMENT This subclone overlaps H21 6_b10 and H21 6_h1.
Sequence submitted by:
Human Genome Center
Lawrence Berkeley Laboratory
Berkeley, CA 94720
e-mail: seq@genome.lbl.gov
The P1, from which this subclone is derived, is adjacent to P1
(1857) and (5005).

FEATURES
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/tissue_lib="Subclones in POT2 from P1 clone H21"
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Best Local Similarity 98.3%; Pred. No. 0;
Matches 2471; Conservative 0; Mismatches 18; Indels 24; Gaps 18;

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DEFINITION
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AUTHORS
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COMMENT
FEATURES
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Best Local Similarity 99.2%; Score 782.8; DB 9; Length 3710;
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LOCUS AX182853
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ACCESSION AX182853
VERSION AX182853.1 GI:15134144
KEYWORDS
SOURCE human.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 700)
AUTHORS Daly,M., Hudson,T.J., Lander,E.S., Rioux,J. and Siminovitch,K.
TITLE Ibd-related polymorphisms
JOURNAL Patent: WO 0142511-A 606 14-JUN-2001;
WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US) ; Ellipsis
Biotherapeutics Corporation (CA)
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LOCUS AX182850
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ACCESSION AX182850
VERSION AX182850.1 GI:15134141
KEYWORDS
SOURCE human.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 700)
AUTHORS Daly,M., Hudson,T.J., Lander,E.S., Rioux,J. and Siminovitch,K.
TITLE Ibd-related polymorphisms
JOURNAL Patent: WO 0142511-A 603 14-JUN-2001;
WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US) ; Ellipsis
Biotherapeutics Corporation (CA)
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XX 20-SEP-1986; 86JP-0223284.
XX (HONJ/) HONJO T.
XX Honjo T, Takatu K, Severinson E;
XX WPI: 1988-085927/13.
DR P-PSDB; AAP81056.
XX
XX
XX Recombinant human B-cell differentiation factor -
PT used for diagnosis or treatment of immuno deficiency diseases,
PT various infections and cancers
XX
XX Example; Fig 5(1)-5(4); 35pp; English.
XX
CC Nucleotide sequence of the exon portions of the human BCDP chromosomal
CC gene completely coincided with the nucleotide sequence of human BCDP
CC cDNA (AAN81380). The BCDP is useful in the diagnosis or treatment of
CC e.g. immunodeficiency diseases occurring due to the deficiency of this
CC factor in a living body and also in the treatment of various infections
CC and cancers.
XX
SQ Sequence 3230 BP; 1027 A; 545 C; 622 G; 1036 T; 0 other;

Query Match 100.0%; Score 3230; DB 9; Length 3230;
- Best Local Similarity 100.0%; Pred. No. 0;
Matches 3230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATCCATAAAGACCCAGTGAACAGAACTCGACCTGCAAGGCTTGCCATTTCCATT 60
DB 1 ATCCATAAAGACCCAGTGAACAGAACTCGACCTGCAAGGCTTGCCATTTCCATT 60
QY 61 CAATCAGTGTCTCCACCAGATTTTCAATTTCTTTAAGACAGATTAATCTAGCCACA 120
DB 61 CAATCAGTGTCTCCACCAGATTTTCAATTTCTTTAAGACAGATTAATCTAGCCACA 120
QY 121 GTCATAGTAGAACAATAGCCGATCTTGAAAAAACATTTCCCAATTTATGTATTTAGC 180
DB 121 GTCATAGTAGAACAATAGCCGATCTTGAAAAAACATTTCCCAATTTATGTATTTAGC 180
QY 181 ATAAATCTGTAGTGTGCTACCTTATCTTTGTTTGACACATCTTTAAGAGAA 240
DB 181 ATAAATCTGTAGTGTGCTACCTTATCTTTGTTTGACACATCTTTAAGAGAA 240
QY 241 GTTAATTTCTGATTTTAAAGAAATGAGGGAATGATGTAATTAACCCAAAGAT 300
DB 241 GTTAATTTCTGATTTTAAAGAAATGAGGGAATGATGTAATTAACCCAAAGAT 300
QY 301 CCTCCGTAATAGAAAATGTTTAAAGGGGGAACAGGATTTTATTATTAAGAT 360
DB 301 CCTCCGTAATAGAAAATGTTTAAAGGGGGAACAGGATTTTATTATTAAGAT 360
QY 361 AAAAGTAATTTATTTTAAAGATTAAGGCAATTTAGTTTACGATATGCC 420
DB 361 AAAAGTAATTTATTTTAAAGATTAAGGCAATTTAGTTTACGATATGCC 420
QY 421 ATTATAGGCAATCTCTATCTGATGTAGAAATTAATTCCTCAAGACAGACAT 480
DB 421 ATTATAGGCAATCTCTATCTGATGTAGAAATTAATTCCTCAAGACAGACAT 480
QY 481 AAATGAGTGGGAGCAGAGTCTGTACTATGCACTTTCTTGCCAAAGGCAACGCAAA 540
DB 481 AAATGAGTGGGAGCAGAGTCTGTACTATGCACTTTCTTGCCAAAGGCAACGCAAA 540
QY 541 CGTTTCAGAGCCATGAGGATGCTTGCATTTGAGTTGCTAGCTCTTGAGGCTGCTAC 600
DB 541 CGTTTCAGAGCCATGAGGATGCTTGCATTTGAGTTGCTAGCTCTTGAGGCTGCTAC 600
QY 601 GTGTATGCAATCCCAAGAAATTCACCAAGTGCATTTGTAAGAGACCTTGCACTG 660

DB 601 GTGTATGCCATCCCAAGAAATTCACCAAGTGCATTTGTAAGAGACCTTGCACTG 660
QY 661 CTTTCTACTCAGCAACTCTGCTGATAGCCAAATGAGGTAATTTCTTTATGATTCCTACA 720
DB 661 CTTTCTACTCAGCAACTCTGCTGATAGCCAAATGAGGTAATTTCTTTATGATTCCTACA 720
QY 721 GTCGTAAAGTCATAGGTAATCATTTGTCATGCTTCCCTTACTATATATAGAGATCTGT 780
DB 721 GTCGTAAAGTCATAGGTAATCATTTGTCATGCTTCCCTTACTATATATAGAGATCTGT 780
QY 781 TATAAATAATAGATTTCTGAGCACAATGATGATGGTGAATTAACATCACCAGCAAC 840
DB 781 TATAAATAATAGATTTCTGAGCACAATGATGATGGTGAATTAACATCACCAGCAAC 840
QY 841 ATTCTGTTAAAGTTATGATGCTGCTGCTGCTGTAATAATGATTTCTCTCTCT 900
DB 841 ATTCTGTTAAAGTTATGATGCTGCTGCTGCTGTAATAATGATTTCTCTCTCT 900
QY 901 CCAGACTCTGAGATTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960
DB 901 CCAGACTCTGAGATTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960
QY 961 AAATGATGGCAGATTAAGTAATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1020
DB 961 AAATGATGGCAGATTAAGTAATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1020
QY 1021 GAACATATTTAATTTCTATATTTGTTTCTATATGCTGCTGCTGCTGCTGCTGCTGCT 1080
DB 1021 GAACATATTTAATTTCTATATTTGTTTCTATATGCTGCTGCTGCTGCTGCTGCTGCT 1080
QY 1081 AAATATGAGGAATGACTTTTATCAAGTAGAATCTTTAAACAAGTGAATGAGGCTCTTT 1140
DB 1081 AAATATGAGGAATGACTTTTATCAAGTAGAATCTTTAAACAAGTGAATGAGGCTCTTT 1140
QY 1141 GGTGATGTTGTTAGTTTCCCTTCCCAAGAGCATGCTGTCAGAGATTTCTCCAGAGAT 1200
DB 1141 GGTGATGTTGTTAGTTTCCCTTCCCAAGAGCATGCTGTCAGAGATTTCTCCAGAGAT 1200
QY 1201 TCCACACTGAGTGAGAGTGGCTGCTAGTCCGTCGAGTTCGACTCTTCTCAGCTTA 1260
DB 1201 TCCACACTGAGTGAGAGTGGCTGCTAGTCCGTCGAGTTCGACTCTTCTCAGCTTA 1260
QY 1261 ACGTGTTCGAAAGTATTTAGCAACTCAGAAATTAATTTTGAACCATGATCAGTAGAC 1320
DB 1261 ACGTGTTCGAAAGTATTTAGCAACTCAGAAATTAATTTTGAACCATGATCAGTAGAC 1320
QY 1321 ATTAATATATTAACAATGCCCCTATATTAATTAATTTCTGATATCTTAATTAATGACT 1380
DB 1321 ATTAATATATTAACAATGCCCCTATATTAATTAATTTCTGATATCTTAATTAATGACT 1380
QY 1381 ATATGATGCTGTATGATGATTAATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1440
DB 1381 ATATGATGCTGTATGATGATTAATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1440
QY 1441 TATTAGTCTAAATAGAAATTAACCTACAGCTAGAACTGTAGAAACACATTTGATGAGTT 1500
DB 1441 TATTAGTCTAAATAGAAATTAACCTACAGCTAGAACTGTAGAAACACATTTGATGAGTT 1500
QY 1501 TAATGTATAATGATTAACACTTCCAAACATTTTTCAGTTCATTAATTAATTAATTAAT 1560
DB 1501 TAATGTATAATGATTAACACTTCCAAACATTTTTCAGTTCATTAATTAATTAATTAAT 1560
QY 1561 CCTTTTAAACCTCTCAGTAATCATTAAGCTTCTACTTTTGAATAATTTATCTT 1620
DB 1561 CCTTTTAAACCTCTCAGTAATCATTAAGCTTCTACTTTTGAATAATTTATCTT 1620
QY 1621 AATATGTGTTGTTGCTAGAAACAAACAAACAAACAAACAAACAAACAAACAAACAAAC 1680
DB 1621 AATATGTGTTGTTGCTAGAAACAAACAAACAAACAAACAAACAAACAAACAAACAAAC 1680
QY 1681 TGTAAATACCAACAAACAAACAAACAAACAAACAAACAAACAAACAAACAAACAAAC 1740
DB 1681 TGTAAATACCAACAAACAAACAAACAAACAAACAAACAAACAAACAAACAAACAAAC 1740

Db 1681 TGTAAATACCAACAAACAGCCCTAATCTTGTGACCAAAATGTTTTAATATATTTT 1740

QY 1741 TTAATGATGATTAATAAGATATATATATTTATTTGTGTACAAATGATGTTTGAAGTAT 1800

Db 1741 TTAATGATGATTAATAAGATATATATATTTATTTGTGTACAAATGATGTTTGAAGTAT 1800

QY 1801 GTATACATGCAAGATGACAAATGACCAAAATTTTATACCTGTCTGATTTATTTGCAT 1860

Db 1801 GTATACATGCAAGATGACAAATGACCAAAATTTTATACCTGTCTGATTTATTTGCAT 1860

QY 1861 TTTAAAAATTTTCCCTCATTTAGCACCAACTGTGCACGAAATCTTTTCAGGGAATAGG 1920

Db 1861 TTTAAAAATTTTCCCTCATTTAGCACCAACTGTGCACGAAATCTTTTCAGGGAATAGG 1920

QY 1921 CACACTGGAGAGTCAAACTGTGCAAGGGGGTACTGTGAAAGACTATTCAAAACTGTGC 1980

Db 1921 CACACTGGAGAGTCAAACTGTGCAAGGGGGTACTGTGAAAGACTATTCAAAACTGTGC 1980

QY 1981 CTTAATAAAGAAATACATTTGACGGGCCAAAAAGTAACTTACACACATTCATGGAAGCTAT 2040

Db 1981 CTTAATAAAGAAATACATTTGACGGGCCAAAAAGTAACTTACACACATTCATGGAAGCTAT 2040

QY 2041 ATTTGCTGCTGTGCTTATTTCTATGGAATTTGACAGTTTCTCTAATACCTATTTGCA 2100

Db 2041 ATTTGCTGCTGTGCTTATTTCTATGGAATTTGACAGTTTCTCTAATACCTATTTGCA 2100

QY 2101 TTTTCTTTTTCACAGAAAAAGTGTGAGAGAAAGACGGAGATTAACCAATTCCTAG 2160

Db 2101 TTTTCTTTTTCACAGAAAAAGTGTGAGAGAAAGACGGAGATTAACCAATTCCTAG 2160

QY 2161 ACTACCTGCAAGAGTTTCTTGTGTATGAAACACCGAGTGAATATGAAAAAGTTGAGACT 2220

Db 2161 ACTACCTGCAAGAGTTTCTTGTGTATGAAACACCGAGTGAATATGAAAAAGTTGAGACT 2220

QY 2221 AAACCTGTTTGTGACGCCAAAGATTTTGGAGGAGAGACATTTTACTGACAGTGAAT 2280

Db 2221 AAACCTGTTTGTGACGCCAAAGATTTTGGAGGAGAGACATTTTACTGACAGTGAAT 2280

QY 2281 GAGGGCCAAAGAAAGTCAAGGCCCTTAATTTTCAATATATATTAATTTCAAGGGAAGTA 2340

Db 2281 GAGGGCCAAAGAAAGTCAAGGCCCTTAATTTTCAATATATATTAATTTCAAGGGAAGTA 2340

QY 2341 AATATTTCAAGCATCTGACACCTTTGCCAGAAAGCATAAATTTCTTAAATATATTTAG 2400

Db 2341 AATATTTCAAGCATCTGACACCTTTGCCAGAAAGCATAAATTTCTTAAATATATTTAG 2400

QY 2401 ATATCAGATCATTTGAAGTATTTCTCCAGGCCAAATTTGATTAATTTTCTTATTTA 2460

Db 2401 ATATCAGATCATTTGAAGTATTTCTCCAGGCCAAATTTGATTAATTTTCTTATTTA 2460

QY 2461 ACTTAACATTTCTGTAATAATGCTGTAACTTAATAGTATTTAATAATGTTAAGAAATT 2520

Db 2461 ACTTAACATTTCTGTAATAATGCTGTAACTTAATAGTATTTAATAATGTTAAGAAATT 2520

QY 2521 GGTAAATAGTATTTATTTAATGTTATGTTGTTCTAATTAACAAATAATAGACAACCTG 2580

Db 2521 GGTAAATAGTATTTATTTAATGTTATGTTGTTCTAATTAACAAATAATAGACAACCTG 2580

QY 2581 TTCAATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2640

Db 2581 TTCAATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2640

QY 2641 ATGCCAGTTTGGAGGAGGCTGAGACATGTGGCTGAGCATCCCATTTCTCTGAG 2700

Db 2641 ATGCCAGTTTGGAGGAGGCTGAGACATGTGGCTGAGCATCCCATTTCTCTGAG 2700

QY 2701 AAGTCTCAAGTTGCAAGGCACACAGAGGTGAAGTGAATCTAGCAGGACTTAGTGGGA 2760

Db 2701 AAGTCTCAAGTTGCAAGGCACACAGAGGTGAAGTGAATCTAGCAGGACTTAGTGGGA 2760

QY 2761 TGTGGGAGCAGGAGACACAGGAGGAGGTAACCTGTTTCTCTCTACAGTATATCCAG 2820

Db 2761 TGTGGGAGCAGGAGACACAGGAGGAGGTAACCTGTTTCTCTCTACAGTATATCCAG 2820

QY 2821 AACCTGGATGCTCGAAGGTAATGCTAGGGAATTAATGAATGAATGCTGTTCCAGA 2880

Db 2821 AACCTGGATGCTCGAAGGTAATGCTAGGGAATTAATGAATGAATGCTGTTCCAGA 2880

QY 2881 TGAATGTAGAACTAAATGAGTTGTAAAGTCCCTGGAAGAGGATGTGAACCTGTAA 2940

Db 2881 TGAATGTAGAACTAAATGAGTTGTAAAGTCCCTGGAAGAGGATGTGAACCTGTAA 2940

QY 2941 CTAGTCTCTGCCCAGCCTGTGAGAAAGATTTGGCAGATCATCTCATTTGCCAGTATAGAG 3000

Db 2941 CTAGTCTCTGCCCAGCCTGTGAGAAAGATTTGGCAGATCATCTCATTTGCCAGTATAGAG 3000

QY 3001 AGGAAGCCAGAAACCTCTCTGCCAAGGCTGACAGGCTTCTTACCACCTGACCTGCAC 3060

Db 3001 AGGAAGCCAGAAACCTCTCTGCCAAGGCTGACAGGCTTCTTACCACCTGACCTGCAC 3060

QY 3061 CATACCAAAAGGACAGACATGTGTAGGGCAGTCCCATTTAGAAAGACTGAGTTCCGTA 3120

Db 3061 CATACCAAAAGGACAGACATGTGTAGGGCAGTCCCATTTAGAAAGACTGAGTTCCGTA 3120

QY 3121 TTCCCGGGGCGAGGCGACGACCGCCGACAAATCCATTTCTGCTGTTAGGCTATCA 3180

Db 3121 TTCCCGGGGCGAGGCGACGACCGCCGACAAATCCATTTCTGCTGTTAGGCTATCA 3180

QY 3181 GTAGCATCACTAGAGATTTCTGTTTGGAAAACTTCTCTCAAGGATCC 3230

Db 3181 GTAGCATCACTAGAGATTTCTGTTTGGAAAACTTCTCTCAAGGATCC 3230

RESULT 2

AAQ74056

ID AAQ74056 standard; DNA; 3230 BP.

XX AC AAQ74056;

XX DT 29-JAN-1996 (first entry)

XX DE Human interleukin-5.

XX KW Interleukin-5; primer; mRNA; specificity; pharmaceutical; ss.

XX OS Homo sapiens.

XX PN JP07123984-A.

XX PD 16-MAY-1995.

XX PF 05-NOV-1993; 93JP-0275852.

XX PR 05-NOV-1993; 93JP-0275852.

XX PA (HITB) HITACHI CHEM CO LTD.

XX DR WPI; 1995-211627/28.

XX PT A primer for the detection and the determ. of a specific messenger RNA - can detect and determine specific mRNA(s) with high reliability

XX PS Example 22; Page 22-24; 35pp; Japanese.

XX CC AAQ74056 is the human interleukin-5 gene. This gene is amplified by the primers AAQ74031-074032. The primers are used specifically for the detection and isolation of this sequence. They have the advantage of high sensitivity and reliability and are useful in the pharmaceutical industry.

XX SQ Sequence 3230 BP; 1027 A; 545 C; 622 G; 1036 T; 0 other;

Query Match 100.0%; Score 3230; DB 16; Length 3230;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 3230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATCCTAATCAAGACCCCGAGTGAACAGAACTCGACCCTGCCAAGCCTTGGCATTTCCATT 60
Db 1 ATCCTAATCAAGACCCCGAGTGAACAGAACTCGACCCTGCCAAGCCTTGGCATTTCCATT 60
QY 61 CAATCACTGCTCTCCACCGAGTATTTCAATTTCTTTAAGACAGATTAACTAGCCACA 120
Db 61 CAATCACTGCTCTCCACCGAGTATTTCAATTTCTTTAAGACAGATTAACTAGCCACA 120
QY 121 GTCATAGTAGAACATAGCCGATCTTGAAAAAACAATCCCAATATTTATGTATTTAGC 180
Db 121 GTCATAGTAGAACATAGCCGATCTTGAAAAAACAATCCCAATATTTATGTATTTAGC 180
QY 181 ATAAAAATCTGTTAGTGTCTACCTATACCTTTGTTTGACACACATCTTTAAGAGAA 240
Db 181 ATAAAAATCTGTTAGTGTCTACCTATACCTTTGTTTGACACACATCTTTAAGAGAA 240
QY 241 GTTAATTTCTGATTTTAAAGAAATGCGAATGCGGCAATGATTTAAACCAAGATT 300
Db 241 GTTAATTTCTGATTTTAAAGAAATGCGAATGCGGCAATGATTTAAACCAAGATT 300
QY 301 CCTCCGTAATAGAAAAATGTTTTAAAGGGGGGAAACAGGATTTTATTTAAAGAT 360
Db 301 CCTCCGTAATAGAAAAATGTTTTAAAGGGGGGAAACAGGATTTTATTTAAAGAT 360
QY 361 AAAAGTAAATTTATTTTAAAGATTAAGGCATTGGAACATTTAGTTTACGATATGCC 420
Db 361 AAAAGTAAATTTATTTTAAAGATTAAGGCATTGGAACATTTAGTTTACGATATGCC 420
QY 421 ATTATTTAGCAATCTCTATCTGATTTGTAAGAAATTTATTTCTTCAAGACAGACAT 480
Db 421 ATTATTTAGCAATCTCTATCTGATTTGTAAGAAATTTATTTCTTCAAGACAGACAT 480
QY 481 AAATTTGACCTGGGAGCGCAGCTCTGTAATGCACTTTCTTTGCCAAAGGCAACGCGAGA 540
Db 481 AAATTTGACCTGGGAGCGCAGCTCTGTAATGCACTTTCTTTGCCAAAGGCAACGCGAGA 540
QY 541 CGTTTCAGAGCCATGAGGATGCTTCTGCAATTTGAGTTTGCTAGCTCTTGAGCTGCTAC 600
Db 541 CGTTTCAGAGCCATGAGGATGCTTCTGCAATTTGAGTTTGCTAGCTCTTGAGCTGCTAC 600
QY 601 GTGTATGCCATCCCAAGAAATGCCAAGTGCATTTGTTGGAAGAGACCTTGGCAGT 660
Db 601 GTGTATGCCATCCCAAGAAATGCCAAGTGCATTTGTTGGAAGAGACCTTGGCAGT 660
QY 661 CTTTCTACTCATCGAACTCTGCTGATAGCCCAATGAGTAATTTCTTTATGATTCCTACA 720
Db 661 CTTTCTACTCATCGAACTCTGCTGATAGCCCAATGAGTAATTTCTTTATGATTCCTACA 720
QY 721 GTCGTAAAGTCATAGTAATCATTTGTGATGTTCTTCTTACTATATATAGAGATCTGT 780
Db 721 GTCGTAAAGTCATAGTAATCATTTGTGATGTTCTTCTTACTATATATAGAGATCTGT 780
QY 781 TATAAATATTAAGATTTCTGAGCACATTTAGTACATGGGTGATTAACATCACAGCAAAAC 840
Db 781 TATAAATATTAAGATTTCTGAGCACATTTAGTACATGGGTGATTAACATCACAGCAAAAC 840
QY 841 ATCTGTAAAAAGTTATGAATGCTGTGCTGTAAAAAATGATTTGATTTCTTCTCT 900
Db 841 ATCTGTAAAAAGTTATGAATGCTGTGCTGTAAAAAATGATTTGATTTCTTCTCTCT 900
QY 901 CCAGACTCTGAGGATTCCTGTTCTGTACATAAAAATGTAAGTAAATTAATGATTCAGTA 960
Db 901 CCAGACTCTGAGGATTCCTGTTCTGTACATAAAAATGTAAGTAAATTAATGATTCAGTA 960
QY 961 AAATGATGCAATGAATTAAGTAAATTTCTGTTTAAAGCTGTAATCATTTAGTTATCATG 1020
Db 961 AAATGATGCAATGAATTAAGTAAATTTCTGTTTAAAGCTGTAATCATTTAGTTATCATG 1020
QY 1021 GAACATATTAATTTCTATATTTGTTTCAATATGCTGCTGGAATGCTGTACTTAT 1080
Db 1021 GAACATATTAATTTCTATATTTGTTTCAATATGCTGCTGGAATGCTGTACTTAT 1080

QY 1081 AAATATGAGAAATGACTTTTATCAAGTAAATCCTTTAAACAAAGTGATTAGCTCTTT 1140
Db 1081 AAATATGAGAAATGACTTTTATCAAGTAAATCCTTTAAACAAAGTGATTAGCTCTTT 1140
QY 1141 GGTGATGTTGTTAGTTTGCCCTTCCCAAGACATCGTGTACAGATTTCTTCCAGAAGAT 1200
Db 1141 GGTGATGTTGTTAGTTTGCCCTTCCCAAGACATCGTGTACAGATTTCTTCCAGAAGAT 1200
QY 1201 TCCACACTGAGTGAGAGGTGCGTGTAGTCTCCGTGACGTTCTGACTCTTCTCAGCTTA 1260
Db 1201 TCCACACTGAGTGAGAGGTGCGTGTAGTCTCCGTGACGTTCTGACTCTTCTCAGCTTA 1260
QY 1261 ACGTGTCTGAAAGTATTTAGCAACTCAGAAATTTATTTTGAACCATGATCAGTAGAC 1320
Db 1261 ACGTGTCTGAAAGTATTTAGCAACTCAGAAATTTATTTTGAACCATGATCAGTAGAC 1320
QY 1321 ATTAATAATATTAACAATGCCCTATATTAATTTCTGATATTTAAATATATATAGCT 1380
Db 1321 ATTAATAATATTAACAATGCCCTATATTAATTTCTGATATTTAAATATATATAGCT 1380
QY 1381 ATATGATGCTGTATGCAATTTGAATATGCGTGTATATTTAAATGTAATATATAGCT 1440
Db 1381 ATATGATGCTGTATGCAATTTGAATATGCGTGTATATTTAAATGTAATATATAGCT 1440
QY 1441 TATTAGTCTAAATAGAAATTAACACTACAGCTAGAACTGTAGAAACACATTTGATAGCT 1500
Db 1441 TATTAGTCTAAATAGAAATTAACACTACAGCTAGAACTGTAGAAACACATTTGATAGCT 1500
QY 1501 TAATGATATATGCAATTTACACTTCCAAACATTTTTCAGTTACATTAATTAAGTATAT 1560
Db 1501 TAATGATATATGCAATTTACACTTCCAAACATTTTTCAGTTACATTAATTAAGTATAT 1560
QY 1561 CCTTTATAAATCTCTCAGTAATCATATATAGCTTCTACTTTTGAATAATTTATCTT 1620
Db 1561 CCTTTATAAATCTCTCAGTAATCATATATAGCTTCTACTTTTGAATAATTTATCTT 1620
QY 1621 AATATGTGTGTTGTTGCTTAGAAACAAACAAACAACTCTTTGAGAGAAAGGAACTCA 1680
Db 1621 AATATGTGTGTTGTTGCTTAGAAACAAACAAACAACTCTTTGAGAGAAAGGAACTCA 1680
QY 1681 TGTAAATACCAACAAACAAAGCCTAATCTTTGTGGAACCAAAATTTGTTAATTAATTTT 1740
Db 1681 TGTAAATACCAACAAACAAAGCCTAATCTTTGTGGAACCAAAATTTGTTAATTAATTTT 1740
QY 1741 TTAATTTGATTAATTAAGTATATATATTTATTTGTTACAAATATGATTTTGAAGTAT 1800
Db 1741 TTAATTTGATTAATTAAGTATATATATTTATTTGTTACAAATATGATTTTGAAGTAT 1800
QY 1801 GTATACATTTGAGAAATGACAATGGAACCAATTTTATACCTTGTCTGATTTATTTGAT 1860
Db 1801 GTATACATTTGAGAAATGACAATGGAACCAATTTTATACCTTGTCTGATTTATTTGAT 1860
QY 1861 TTTAAAAATTTCTCATTTAGCACCAACTGTGCACTGAAGAAATCTTTCAGGAATAGG 1920
Db 1861 TTTAAAAATTTCTCATTTAGCACCAACTGTGCACTGAAGAAATCTTTCAGGAATAGG 1920
QY 1921 CACACTGAGAGTCAAACTGTGCAAGGGGTACTGTGAAAGACATTTCAAAAACTTGTG 1980
Db 1921 CACACTGAGAGTCAAACTGTGCAAGGGGTACTGTGAAAGACATTTCAAAAACTTGTG 1980
QY 1981 CTTAATAAAGAAATTAATTTGACGGCCAAAAAGTAACTTACACACATTTCAATGGAAGCTAT 2040
Db 1981 CTTAATAAAGAAATTAATTTGACGGCCAAAAAGTAACTTACACACATTTCAATGGAAGCTAT 2040
QY 2041 ATTTGCTCTGCTGCTGCTATTTCTATGGAATTTGACAGTTTCCGTGTAATACCTATTTGCA 2100
Db 2041 ATTTGCTCTGCTGCTGCTATTTCTATGGAATTTGACAGTTTCCGTGTAATACCTATTTGCA 2100
QY 2101 TTTTCTTTTTCACAGAAAAAGTGTGAGAGAAAGACGAGAGATTAACCAATTTCTAG 2160
Db 2101 TTTTCTTTTTCACAGAAAAAGTGTGAGAGAAAGACGAGAGATTAACCAATTTCTAG 2160
QY 2161 ACTACCTGCAAGAGTTTCTTGTGTAATGAACACCGAGTGATTAATGAAGTTGAGACT 2220

Db	2161	ACTACCTGCAGAGTTCCTTGCTGTATGAAACACCGAGTGGATAATAGAAAGTTGAGACT	2220
QY	2221	AAACTGCTTTGTTGGACGCCAAAGATTTTGGAGGAGAGACATTTTACTGCAGTGAGAAAT	2280
Db	2221	AAACTGGTTTGTTCAGACCCAAAGATTTTGGAGGAGAGACATTTTACTGCAGTGAGAAAT	2280
QY	2281	GAGGGCCAGAAAGAGTGCAGCCCTTAATTTTCAATATAATTTAACTTCAGAGGAAAGTA	2340
Db	2281	GAGGGCCAGAAAGAGTGCAGCCCTTAATTTTCAATATAATTTAACTTCAGAGGAAAGTA	2340
QY	2341	AATATTTTCAGGCATACTGCACACTTTGCCAGAAAGCATAAATTTCTTAAATATATTTTCAG	2400
Db	2341	AATATTTTCAGGCATACTGCACACTTTGCCAGAAAGCATAAATTTCTTAAATATATTTTCAG	2400
QY	2401	ATATCAGAATCATTGAACTATTTTCCCTCCAGCGCAAAATTGATATACTTTTCTTATTTTA	2460
Db	2401	ATATCAGAATCATTGAACTATTTTCCCTCCAGCGCAAAATTGATATACTTTTCTTATTTTA	2460
QY	2461	ACTTAACATTTCTGTAAATGTCCTGTTAACTTAATAGTATTTATGAAATGGTTAAGAAATT	2520
Db	2461	ACTTAACATTTCTGTAAATGTCCTGTTAACTTAATAGTATTTATGAAATGGTTAAGAAATT	2520
QY	2521	GGTAAATTAGTATTTATTTAATGTTATGTTGTGTCTAATTAACAAAAATAGACAACTG	2580
Db	2521	GGTAAATTAGTATTTATTTAATGTTATGTTGTGTCTAATTAACAAAAATAGACAACTG	2580
QY	2581	TTCAATTTGCTGCTGCGCTCTGTCCTTAGCAATTTGAAAGTTAGCACAGATCCCATTTGAGTAC	2640
Db	2581	TTCAATTTGCTGCTGCGCTCTGTCCTTAGCAATTTGAAAGTTAGCACAGATCCCATTTGAGTAC	2640
QY	2641	ATGCCAGTTTGGAGGAAGGCTCTGAGCACACATGCGCTGAGCATCCCATTTCTCTGGAG	2700
Db	2641	ATGCCAGTTTGGAGGAAGGCTCTGAGCACACATGCGCTGAGCATCCCATTTCTCTGGAG	2700
QY	2701	AAGTCTCAAGGTTGCAAGGCACACACAGAGGTGGAAGTGATCTAGCAGACTTAGTGGGGA	2760
Db	2701	AAGTCTCAAGGTTGCAAGGCACACACAGAGGTGGAAGTGATCTAGCAGACTTAGTGGGGA	2760
QY	2761	TGTGGGAGCAGGACACACAGGCAAGAGGTGAACCTGGTTTTCTCTCTACAGTATATCCAG	2820
Db	2761	TGTGGGAGCAGGACACACAGGCAAGAGGTGAACCTGGTTTTCTCTCTACAGTATATCCAG	2820
QY	2821	AACTGGGATGTTCCAAAGGGTAAATGTTAGGGAATAATGAATGAATGATGTTTCCAAGA	2880
Db	2821	AACTGGGATGTTCCAAAGGGTAAATGTTAGGGAATAATGAATGAATGATGTTTCCAAGA	2880
QY	2881	TGATTTAGAACTTAAATGAGTTGTAAGTCTCCCTGGAAGGAAGGATGGAACCTGTAA	2940
Db	2881	TGATTTAGAACTTAAATGAGTTGTAAGTCTCCCTGGAAGGAAGGATGGAACCTGTAA	2940
QY	2941	CTAGGTTCTGCCACGCTGTGAGAAAGAAATTTGGCAGATCATCTCATGGCAGTATAGAG	3000
Db	2941	CTAGGTTCTGCCACGCTGTGAGAAAGAAATTTGGCAGATCATCTCATGGCAGTATAGAG	3000
QY	3001	AGGAAGCCAGAAACCCTCTCTGCCAAGGCTGCAGGGGTTCTTACCACCTGACCCTGCAC	3060
Db	3001	AGGAAGCCAGAAACCCTCTCTGCCAAGGCTGCAGGGGTTCTTACCACCTGACCCTGCAC	3060
QY	3061	CATAACAAAAGACAGAGACATGTTAGGCGAGTCCCATTAGAAAGACTGAGTCCGTA	3120
Db	3061	CATAACAAAAGACAGAGACATGTTAGGCGAGTCCCATTAGAAAGACTGAGTCCGTA	3120
QY	3121	TTCCCGGGGACAGGCGACACAGGCGCGACACATCCATTTCTGCGTCTTATGGCTATCA	3180
Db	3121	TTCCCGGGGACAGGCGACACAGGCGCGACACATCCATTTCTGCGTCTTATGGCTATCA	3180
QY	3181	GTAGCATCACTAGAGATTTCTTGTGTGAGAAAACCTTCTCTCAAGGATCC 3230	
Db	3181	GTAGCATCACTAGAGATTTCTTGTGTGAGAAAACCTTCTCTCAAGGATCC 3230	

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AAC73725
ID  AAC73725 standard; DNA; 3230 BP.
XX
AC  AAC73725;
XX
DT  02-FEB-2001 (first entry)
XX
DE  Human IL-5 nucleotide sequence.
XX
KW  Human; interleukin-5; IL-5; signal transduction;
KW  antisense oligonucleotide; antiasthmatic; immunosuppressive; cytostatic;
KW  IL-5 receptor-alpha; asthma; eosinophilic syndrome; infection;
KW  inflammation; cancer; ds.
XX
OS  Homo sapiens.
XX
PN  WO200058512-A1.
XX
PD  05-OCT-2000.
XX
PF  17-MAR-2000; 2000WO-US07318.
XX
PR  26-MAR-1999; 99US-0280799.
XX
PA  (ISIS-) ISIS PHARM INC.
XX
PI  Dean NM, Karras JG, McKay R;
XX
DR  WPI; 2000-594648/56.
XX
PT  Antisense oligonucleotide compound used to treat asthma and
PT  eosinophilic syndrome in humans modulates interleukin-5 signal
PT  transduction -
XX
XX  Example 22; Page 127-128; 156pp; English.
XX
CC  The present sequence was used to design oligonucleotides for antisense
CC  modulation of interleukin-5 (IL-5) signal transduction. Oligonucleotides
CC  were designed to target nucleic acids encoding IL-5 and IL-5
CC  receptor-alpha. The antisense oligonucleotides may be used for the
CC  treatment of diseases associated with IL-5 signal transduction, IL-5
CC  expression or IL-5 receptor-alpha expression. Such diseases include
CC  asthma and eosinophilic syndrome. The oligonucleotides are also useful
CC  for research uses and to prevent or delay infection, inflammation or
CC  tumour formation.
XX
SQ  Sequence 3230 BP; 1027 A; 545 C; 622 G; 1036 T; 0 other;

Query Match          100.0%; Score 3230; DB 21; Length 3230;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1  ATCCTAATCAAGACCCCGAGTGAACAGAACTCGACCCCTGCCAAGGCTTGGCATTTCATTT 60
   |||||||
DB  1  ATCCTAATCAAGACCCCGAGTGAACAGAACTCGACCCCTGCCAAGGCTTGGCATTTCATTT 60
QY  61  CAATCACTGTCTTCCACCCAGTAGTATTTTCAATTTCTTTTAAGACAGATTAACTAGCCACA 120
   |||||||
DB  61  CAATCACTGTCTTCCACCCAGTAGTATTTTCAATTTCTTTTAAGACAGATTAACTAGCCACA 120
QY  121  GTCATAGTAGAACATAGCCGATCTGAAAAAAAACATTCCTCAATTTATGTATTTAGC 180
   |||||||
DB  121  GTCATAGTAGAACATAGCCGATCTGAAAAAAAACATTCCTCAATTTATGTATTTAGC 180
QY  181  ATAAAAATTTCTGTTAGTGTCTACCTTATCTTTGTTTGCACACATCTTTTAAGAGAA 240
   |||||||
DB  181  ATAAAAATTTCTGTTAGTGTCTACCTTATCTTTGTTTGCACACATCTTTTAAGAGAA 240
QY  241  GTTAATTTTCTGATTTTAAAGAAATGCAAAATGTGGGCAATGATGTATTAACCCAAAGATT 300
   |||||||
DB  241  GTTAATTTTCTGATTTTAAAGAAATGCAAAATGTGGGCAATGATGTATTAACCCAAAGATT 300
QY  301  CCTCCGTAATAGAAAATGTTTTTAAAGGGGGGGAACAGGGATTTTATTATTAAAAAGAT 360

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|||||
Db 301 CCTCCGTAATAGAAAAATGTTTTAAAGGGGGGAAACAGGATTTTATATATATAAAGAT 360
QY 361 AAAAGTAAATTTATTTTAAAGATATAGGCATTTGAAACATTTAGTTTACAGATATGCC 420
Db 361 AAAAGTAAATTTATTTTAAAGATATAGGCATTTGAAACATTTAGTTTACAGATATGCC 420
QY 421 ATATATAGGCATTTCTATATGATTTGTAGAAAATATTCATTTCTTCAAGACAGACAAT 480
Db 421 ATATATAGGCATTTCTATATGATTTGTAGAAAATATTCATTTCTTCAAGACAGACAAT 480
QY 481 AAAATGACTGGGACGACGCTGTACTATGACATTTCTTTGCCAAAGGCAACGCAAGAA 540
Db 481 AAAATGACTGGGACGACGCTGTACTATGACATTTCTTTGCCAAAGGCAACGCAAGAA 540
QY 541 CGTTTCAGAGCCATGAGATGCTTCTGCATTTGAGTTTGTAGCTCTTGAGCTGCTTAC 600
Db 541 CGTTTCAGAGCCATGAGATGCTTCTGCATTTGAGTTTGTAGCTCTTGAGCTGCTTAC 600
QY 601 GTGTATGCCATCCCCACAGAAATTTCCACAGAGTGCATTTGTGAAGAGACCTTGGCACTG 660
Db 601 GTGTATGCCATCCCCACAGAAATTTCCACAGAGTGCATTTGTGAAGAGACCTTGGCACTG 660
QY 661 CTTTCTACTCATCGAACCTGTGCTGATAGCCCAATGAGTAATTTCTTATGATTCCTACA 720
Db 661 CTTTCTACTCATCGAACCTGTGCTGATAGCCCAATGAGTAATTTCTTATGATTCCTACA 720
QY 721 GTCTGTAAGTGATAGTAATCATTTGTGATGTTCTTACTATATATAGAGATCTGT 780
Db 721 GTCTGTAAGTGATAGTAATCATTTGTGATGTTCTTACTATATATAGAGATCTGT 780
QY 781 TATATAATATATAGATTTCTGAGACATTTAGTACATGGTGATTAATCATCACACAGCAAA 840
Db 781 TATATAATATATAGATTTCTGAGACATTTAGTACATGGTGATTAATCATCACACAGCAAA 840
QY 841 ATCTGTTTAAAGTTATGAAATGCTGTGCTGTAAAAATGATTTCTTCTTCTCTCT 900
Db 841 ATCTGTTTAAAGTTATGAAATGCTGTGCTGTAAAAATGATTTCTTCTTCTCTCT 900
QY 901 CCAGACTCTGAGGATTTCTGTCTGTACATATAAAATGTAAATTTATGATTCAGTA 960
Db 901 CCAGACTCTGAGGATTTCTGTCTGTACATATAAAATGTAAATTTATGATTCAGTA 960
QY 961 AAATGATGCGATGATTAAGTAATTTCTCTGTTTTAAAGCTGTAATCATAGTATCATTTG 1020
Db 961 AAATGATGCGATGATTAAGTAATTTCTCTGTTTTAAAGCTGTAATCATAGTATCATTTG 1020
QY 1021 GAACATAATTTTCTATATTTTGTTCATATGCTGCTGTAATGCTGTACTTTAT 1080
Db 1021 GAACATAATTTTCTATATTTTGTTCATATGCTGCTGTAATGCTGTACTTTAT 1080
QY 1081 AAATATGAGGAATGACTTTTATCAAGTAGAATCTTTTAAACAAGTGATTAAGCTCTTT 1140
Db 1081 AAATATGAGGAATGACTTTTATCAAGTAGAATCTTTTAAACAAGTGATTAAGCTCTTT 1140
QY 1141 GGTGATGTGTAGTTTGGCTTCCCAAAGAGCATGCTGTCAGGATTTCTTCCAGAGGAT 1200
Db 1141 GGTGATGTGTAGTTTGGCTTCCCAAAGAGCATGCTGTCAGGATTTCTTCCAGAGGAT 1200
QY 1201 TCCACACTGAGTGAGAGTGCGTCTAGTCTCCGTGACATTTCTGACTCTTCTCACTCTA 1260
Db 1201 TCCACACTGAGTGAGAGTGCGTCTAGTCTCCGTGACATTTCTGACTCTTCTCACTCTA 1260
QY 1261 ACGTGTCTGAAAGTATTAGCAACTCAGAAATATATTTTGAACCATGATCAGTAGAC 1320
Db 1261 ACGTGTCTGAAAGTATTAGCAACTCAGAAATATATTTTGAACCATGATCAGTAGAC 1320
QY 1321 ATTAATAATATATTAACAATGCCCTATATTAATTTCTGATTAATTAATTAATGACT 1380
Db 1321 ATTAATAATATATTAACAATGCCCTATATTAATTTCTGATTAATTAATTAATGACT 1380
QY 1381 ATATGATGCTGTATGATTAATGATGCTGCTGCTATTAATTAATTAATTAATGACT 1440
Db 1381 ATATGATGCTGTATGATTAATGATGCTGCTGCTATTAATTAATTAATTAATGACT 1440

Db 1381 ATATGATGCTGTATGATTAATGATGCTGCTGCTATTAATTAATTAATTAATGACT 1440
QY 1441 TATAGCTAAATAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATGACT 1500
Db 1441 TATAGCTAAATAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATGACT 1500
QY 1501 TAATGATATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATGACT 1560
Db 1501 TAATGATATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATGACT 1560
QY 1561 CCTTATTAATACTCTCAGTAATCATATTAAGCTTCATCTTTTGAATTTTATCTT 1620
Db 1561 CCTTATTAATACTCTCAGTAATCATATTAAGCTTCATCTTTTGAATTTTATCTT 1620
QY 1621 AATATGT 1680
Db 1621 AATATGT 1680
QY 1681 TGTAAATACCAAAACAAAGCCCTAATTTGTGTGACCAAAATTTTAAATTAATTTT 1740
Db 1681 TGTAAATACCAAAACAAAGCCCTAATTTGTGTGACCAAAATTTTAAATTAATTTT 1740
QY 1741 TTAATGATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATGACT 1800
Db 1741 TTAATGATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATGACT 1800
QY 1801 GTATACATTTGAGAAATGACAAATGACCAAAATTTTATACCTGTGTGTGTGTGTGTGTGT 1860
Db 1801 GTATACATTTGAGAAATGACAAATGACCAAAATTTTATACCTGTGTGTGTGTGTGTGTGT 1860
QY 1861 TTTAAATTTTCTCTCATTTAGCACCAACTGTGCACCTGAAGAAATCTTTCAGGGAATAGG 1920
Db 1861 TTTAAATTTTCTCTCATTTAGCACCAACTGTGCACCTGAAGAAATCTTTCAGGGAATAGG 1920
QY 1921 CACACTGAGAGTCAAACTGTGTGCAAGGGGTACTGTGGAAGAACTATTCAAAACTGTCTC 1980
Db 1921 CACACTGAGAGTCAAACTGTGTGCAAGGGGTACTGTGGAAGAACTATTCAAAACTGTCTC 1980
QY 1981 CTTAATAAAGAAATACATTTGACGGGCCAAAGTAAGTTACACACATTCATTAAGGAGCTAT 2040
Db 1981 CTTAATAAAGAAATACATTTGACGGGCCAAAGTAAGTTACACACATTCATTAAGGAGCTAT 2040
QY 2041 ATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2100
Db 2041 ATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2100
QY 2101 TTTTCTTTTTCACAGAAAAAGTGTGAGAAAGAAAGAGAGAGTAACCAATTCCTAG 2160
Db 2101 TTTTCTTTTTCACAGAAAAAGTGTGAGAAAGAAAGAGAGTAACCAATTCCTAG 2160
QY 2161 ACTACCTGCAAGAGTTTCTTGTGTATGAACACCGAGTGGATTAAGAAAGTTGAGACT 2220
Db 2161 ACTACCTGCAAGAGTTTCTTGTGTATGAACACCGAGTGGATTAAGAAAGTTGAGACT 2220
QY 2221 AAACCTGTTTGTGACAGCCAAAGATTTTGAGAGAGAGAGACATTTTACTGACGTGAGAT 2280
Db 2221 AAACCTGTTTGTGACAGCCAAAGATTTTGAGAGAGAGAGACATTTTACTGACGTGAGAT 2280
QY 2281 GAGGGCCAAAGAGAGTCAAGCCCTTAATTTTCAATATTAATTTCACTCAGAGGGAAGTA 2340
Db 2281 GAGGGCCAAAGAGAGTCAAGCCCTTAATTTTCAATATTAATTTCACTCAGAGGGAAGTA 2340
QY 2341 AATATTTCAAGCATTAATTAATTTTCACTTTCAGAGAAAGCATAAATTTTATATTTTCAAG 2400
Db 2341 AATATTTCAAGCATTAATTAATTTTCACTTTCAGAGAAAGCATAAATTTTATATTTTCAAG 2400
QY 2401 ATATCAGAAATTAAGTATTTTCTTCCAGGCAAAATTTGATTAATTTTCTTCTTCTTCTTCT 2460
Db 2401 ATATCAGAAATTAAGTATTTTCTTCCAGGCAAAATTTGATTAATTTTCTTCTTCTTCTTCT 2460
QY 2461 ACTTAACATTTCTTAATAATGTCTGTAACTTAATTAATTAATTAATTAATTAATTAATTAAT 2520
Db 2461 ACTTAACATTTCTTAATAATGTCTGTAACTTAATTAATTAATTAATTAATTAATTAATTAAT 2520

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OY 2521 GGTAAATAGTATTTATTTAATGTTATGTTGTTCTTAATAAACAATAATAGACAACGTG 2580
    |||||||
Db 2521 GGTAAATAGTATTTATTTAATGTTATGTTGTTCTTAATAAACAATAATAGACAACGTG 2580
OY 2581 TTCAATTGCTGCTGGCCTCTGCTTACCAATTTGAAGTTAGCACACAGTCCATTTAGTAC 2640
    |||||||
Db 2581 TTCAATTGCTGCTGGCCTCTGCTTACCAATTTGAAGTTAGCACACAGTCCATTTAGTAC 2640
OY 2641 ATGCCAGTTTGGAGGAAGGTTGAGCACATGTGCTGAGCATCCCATTTCTCTGGAG 2700
    |||||||
Db 2641 ATGCCAGTTTGGAGGAAGGTTGAGCACATGTGCTGAGCATCCCATTTCTCTGGAG 2700
OY 2701 AAGTCTCAAGTTTGAAGGACACACAGGAGGTTGAAGTGAATGATTAAGCAGACTTACTGGGA 2760
    |||||||
Db 2701 AAGTCTCAAGTTTGAAGGACACACAGGAGGTTGAAGTGAATGATTAAGCAGACTTACTGGGA 2760
OY 2761 TGTGGGAGCAGGACACACAGGAGGTTGAACCTGTTTCTCTACAGTATATCAG 2820
    |||||||
Db 2761 TGTGGGAGCAGGACACACAGGAGGTTGAACCTGTTTCTCTACAGTATATCAG 2820
OY 2821 AACCTGGATGTCGAAAGGTTAAATGTTAGGAATGAATGAATGTCGTTTCCAGA 2880
    |||||||
Db 2821 AACCTGGATGTCGAAAGGTTAAATGTTAGGAATGAATGAATGTCGTTTCCAGA 2880
OY 2881 TGATTTAGAACTAAATGATTTGTAAGCTCCCTGGAAGAGGATGTGAACCTGTAA 2940
    |||||||
Db 2881 TGATTTAGAACTAAATGATTTGTAAGCTCCCTGGAAGAGGATGTGAACCTGTAA 2940
OY 2941 CTAGTTCTTCCCTGAGCCTGTGAGAAGATTTGGCAGATCATCTCATTTGCCAGTATAGAG 3000
    |||||||
Db 2941 CTAGTTCTTCCCTGAGCCTGTGAGAAGATTTGGCAGATCATCTCATTTGCCAGTATAGAG 3000
OY 3001 AGGAAGCCAGAAACCTCTCTGCAAGGCTTGAAGGGTCTTACCACCTGACCTGCAC 3060
    |||||||
Db 3001 AGGAAGCCAGAAACCTCTCTGCAAGGCTTGAAGGGTCTTACCACCTGACCTGCAC 3060
OY 3061 CATACAAAAGGACAGAGAGATGTTAGGCGAGTCCCATTTAGAAAGACTGAGTTCCGTA 3120
    |||||||
Db 3061 CATACAAAAGGACAGAGAGATGTTAGGCGAGTCCCATTTAGAAAGACTGAGTTCCGTA 3120
OY 3121 TTCCCGGGGCGAGGCGAGCAGCAGCCGACACACATCCATTCCTGCTTATGGCTATCA 3180
    |||||||
Db 3121 TTCCCGGGGCGAGGCGAGCAGCAGCCGACACACATCCATTCCTGCTTATGGCTATCA 3180
OY 3181 GTAGCATCACTAGAGATTTCTTGTGAGAAACTTCTCTCAAGGATCC 3230
    |||||||
Db 3181 GTAGCATCACTAGAGATTTCTTGTGAGAAACTTCTCTCAAGGATCC 3230

RESULT 4
AAS15002
ID AAS15002 standard; DNA; 9738 BP.
XX
AC AAS15002;
XX
DT 14-FEB-2002 (first entry)
XX
DE DNA encoding interleukin 5 (IL5).
XX
KW Human; interleukin 5; IL5; antiinflammatory; antiasthmatic; asthma;
KW haplotyping; inflammatory disorder; single nucleotide polymorphism;
KW SNP; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 4071..5738
FT /tag= a
FT /product= "Interleukin 5"
FT /note= "The CDS is specifically claimed in claim 24"
FT variation replace (3325,C)
FT /*tag= b
```

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FT variation /standard_name= "Single nucleotide polymorphism"
FT replace (3430,G)
FT /*tag= c
FT /standard_name= "Single nucleotide polymorphism"
FT replace (3453,A)
FT /*tag= d
FT /standard_name= "Single nucleotide polymorphism"
FT replace (3825,A)
FT /*tag= e
FT /standard_name= "Single nucleotide polymorphism"
FT 4071..4214
FT /*tag= f
FT /number= 1
FT 4215..4422
FT /*tag= g
FT /number= 1
FT replace (4359,G)
FT /*tag= h
FT /standard_name= "Single nucleotide polymorphism"
FT 4423..4455
FT /*tag= i
FT /number= 2
FT 4456..5405
FT /*tag= j
FT /number= 2
FT replace (5389,T)
FT /*tag= k
FT /standard_name= "Single nucleotide polymorphism"
FT 5406..5534
FT /*tag= l
FT /number= 3
FT 5535..5639
FT /*tag= m
FT /number= 3
FT replace (5507,C)
FT /*tag= n
FT /standard_name= "Single nucleotide polymorphism"
FT 5640..5738
FT /*tag= o
FT /number= 4
FT replace (5717,A)
FT /*tag= p
FT /standard_name= "Single nucleotide polymorphism"

WO200177132-A2.
18-OCT-2001.
PD
11-APR-2001; 2001WO-US12011.
PF
XX
PR 11-APR-2000; 2000US-196250P.
PR
XX
PA (GENA-) GENAISSANCE PHARM INC.
XX
PI Bentivegna SC, Chew A, Choi JY, Denton RR, Kazemi A, Nandabalan K;
PI Parks KE;
PI
XX
DR WPI; 2002-041289/05.
DR P-PSDB; AAU10353.
XX
PT New haplotypes of the human interleukin 5 gene, useful to diagnose and
PT treat diseases associated with the gene including inflammatory
PT disorders such as asthma
XX
PS Claim 19; Fig 1; 65pp; English.
XX
CC The invention relates to haplotyping the human interleukin 5 (IL5) gene
CC of an individual, comprising determining if the individual has one of the
CC IL5 haplotypes or haplotype pairs fully defined in the specification.
CC Haplotyping the IL5 gene of an individual, comprises determining the
CC identity of the nucleotide at two or more polymorphic sites in one copy
CC of the gene. The method also involves identifying an association between
CC a trait and a haplotype or haplotype pair of the IL5 gene, comprising
```


CC comparing the frequency of the haplotype/pair in a population exhibiting
CC the trait with that of a reference population. A higher frequency in the
CC trait population indicates the trait is associated with the haplotype.
CC The polynucleotides and screened compounds are useful to develop
CC treatment for diseases associated with IL-5 activity including
CC inflammatory disorders such as asthma. The present sequence represents
CC the coding sequence of interleukin 5 (IL5) as described in the
CC method of the invention.

XX Sequence 9738 BP; 2808 A; 2015 C; 1982 G; 2933 T; 0 other;

Query Match 91.1%; Score 2941.6; DB 24; Length 9738;
Best Local Similarity 98.5%; Pred. No. 0;
Matches 3192; Conservative 0; Mismatches 19; Indels 29; Gaps 21;

QY 1 ATCTTAATCAAGACCCAGTGAACAGAACTGACCCCTGCCAGGCTTGCA-TTTCATT 59
DB 3522 ATCTTAATCAAGACCCAGTGAACAGAACTGACCCCTGCCAGGCTTGCA-TTTCATT 3581
QY 60 TCAATCACTGCTCTCCACACAGATTTTCAATTTCTTTAAGACAGATTAACTAGCCAC 119
DB 3582 TCAATCACTGCTCTCCACACAGATTTTCAATTTCTTTAAGACAGATTAACTAGCCAC 3641
QY 120 AGTCATAGTAGAACATAGCCAGTCTTGAAAAAACAATCCCAATATTATGATTTAG 179
DB 3642 AGTCATAGTAGAACATAGCCAGTCTTGAAAAAACAATCCCAATATTATGATTTAG 3699
QY 180 CATAAATCTCTGTTAGTGTCTACCTTATCTTTGTTGACACACATCTTTAAGAGA 239
DB 3700 CATAAATCTCTGTTAGTGTCTACCTTATCTTTGTTGACACACATCTTTAAGAGA 3759
QY 240 AGTTAATTTCTGATTTTAAAGAAATGCAATGTGGGCAATGATGATTAACCAAGAT 299
DB 3760 AGTTAATTTCTGATTTTAAAGAAATGCAATGTGGGCAATGATGATTAACCAAGAT 3819
QY 300 TCCTCCGTAATAGAAATGTTTTAAAGGGGGGAAACAGGATTTTATTTAAAGA 359
DB 3820 TC-TTCGTAATAGAAATGTTTTAAAGGGGGGAAACAGGATTTTATTTAAAGA 3877
QY 360 TAAAGTAATTTATTTTAAAGTATTAAGGCATTTAGTTCACGATATGC 419
DB 3878 TAAAGTAATTTATTTTAAAGTATTAAGGCATTTAGTTCACGATATGC 3937
QY 420 CATATATAGGCATTTCTCTATCTGATTTAGAAATTTATCTTCTCAAGACAGACA 479
DB 3938 CATATATAGGCATTTCTCTATCTGATTTAGAAATTTATCTTCTCAAGACAGACA 3997
QY 480 TAAATGACTGGGAGCAGTCTGTACTATGACATTTCTTCCAAAGGCAAGCAGAGA 539
DB 3998 TAAATGACTGGGAGCAGTCTGTACTATGACATTTCTTCCAAAGGCAAGCAGAGA 4057
QY 540 ACGTTTCAGAGCCATGAGATGCTTCTGCAATTTGAGTTTCTAGCTCTTGAGCTGCTA 599
DB 4058 ACGTTTCAGAGCCATGAGATGCTTCTGCAATTTGAGTTTCTAGCTCTTGAGCTGCTA 4117
QY 600 CGTGTATGCCATCCCAACAGAAATCCCAAGTGCATTTGGTGAAGAGACCTTGCACT 659
DB 4118 CGTGTATGCCATCCCAACAGAAATCCCAAGTGCATTTGGTGAAGAGACCTTGCACT 4177
QY 660 GCTTCTACTCATCGAATCTGCTGATAGCCAAATGAGTAATTTCTTATGATTCCTAC 719
DB 4178 GCTTCTACTCATCGAATCTGCTGATAGCCAAATGAGTAATTTCTTATGATTCCTAC 4237
QY 720 AGTCTGTAAAGTGCATAGGTAATTTGATGTTCTTCTTACTATATATAGAGATCTG 779
DB 4238 AGTCTGTAAAGTGCATAGGTAATTTGATGTTCTTCTTACTATATATAGAGATCTG 4297
QY 780 TTATATAATTAAGATTTCTGAGACATTTAGTACATGGGTGATTAACATACACAGAAA 839
DB 4298 TTATATAATTAAGATTTCTGAGACATTTAGTACATGGGTGATTAACATACACAGAAA 4357
QY 840 CATCTCTTAAAGTATGAATGCTGCTGCTGTAATAATGATTTCTTCTCTC 899
DB 840 CATCTCTTAAAGTATGAATGCTGCTGCTGTAATAATGATTTCTTCTCTC 899

DB 4358 CATCTGTAAAAAGTTATGAATGCTGCTGCTGTAATAATGATTTCTTCTCTC 4417
QY 900 TCCAGACTCTGAGGATTTCTGTTCTGATCATATAAATGTAAGTTAATGATGACGT 959
DB 4418 TCCAGACTCTGAGGATTTCTGTTCTGATCATATAAATGTAAGTTAATGATGACGT 4477
QY 960 AAAATGATGGCAGTAATAAGTAATAATTTCTGTTTAAAGCTGTAATCATAGTATCAT 1019
DB 4478 AAAATGATGGCAGTAATAAGTAATAATTTCTGTTTAAAGCTGTAATCATAGTATCAT 4537
QY 1020 GGAACATATTAATTTCTATATTTGTTTCTATATGAGGTGGCTGTAATGCTGATCTA 1079
DB 4538 GGAACATATTAATTTCTATATTTGTTTCTATATGAGGTGGCTGTAATGCTGATCTA 4597
QY 1080 TAAATATGAGCAATGACTTTTATCAAGTATGATCTTTAAACAAGTGATAGGCTCTT 1139
DB 4598 TAAATATGAGCAATGACTTTTATCAAGTATGATCTTTAAACAAGTGATAGGCTCTT 4657
QY 1140 TGGTATGTTGTTAGTTGCTTCCCAAGAGCATGCTGCA-GGATTTCTTCCAGAGG 1198
DB 4658 TGGTATGTTGTTAGTTGCTTCCCAAGAGCATGCTGCTGCAAGGATTTCTTCCAGAGG 4716
QY 1199 ATTCACACTGAGTGAAGAGTGGCTGCTAGTCTCCGTCAGTCTGACTCTTCTCAGTC 1258
DB 4717 ATTCACACTGAGTGAAGAGTGGCTGCTAGTCTCCGTCAGTCTGACTCTTCTCAGTC 4776
QY 1259 TAACGTTTCTGAAAGTATTTAGCAACTGAGATTTATTTTAAAGCAACATGATCAGAG 1318
DB 4777 TAACGTTTCTGAAAGTATTTAGCAACTGAGATTTATTTTAAAGCAACATGATCAGAG 4836
QY 1319 ACATTAATAATATTAACAATGCCCCATATTAATAA-TTCTGCACTTAAATAATATAG 1377
DB 4837 ACATTAATAATATTAACAATGCCCCATATTAATAA-TTCTGCACTTAAATAATATAG 4896
QY 1378 ACTATATGATGGTG-TGTATGCAAT--GAATATGCCCTGCTGATATTAATAATGTAATAAT 1434
DB 4897 ACTATATGATGGTGTTGATGCAATTTGAATATGCTGCTGCTGATATTAATAATGTAATAAT 4956
QY 1435 ATAG-TTATATAGTCTAATAATAGAAATTAACACTACAGCTAGAACGTGTAAGAACATATGAT 1493
DB 4957 ATAGTTTATATAGTCTAATAATAGAAATTAACACTACAGCTAGAACGTGTAAGAACATATGAT 5016
QY 1494 ATGAGTTTATATGATTAATGATTTACACTTCCAAACATTTTTCAGTTACATATTA 1553
DB 5017 ATGAGTTTATATGATTAATGATTTACACTTCCAAACATTTTTCAGTTACATATTA 5076
QY 1554 GTTATATCTTTATTAATAACTCTCAGTAATCATATTAAGCTTCACTCTTTTGAATAAT 1613
DB 5077 GTTATATCTTTATTAATAACTCTCAGTAATCATATTAAGCTTCACTCTTTTGAATAAT 5136
QY 1614 TTATCTTAATATGTTGTTGTTGCTAGAAACAAACAAACAAACAACTCTTTGGAGAGG 1673
DB 5137 TTATCTTAATATGTTGTTGTTGCTAGAAACAAACAAACAAACAACTCTTTGGAGAGG 5196
QY 1674 GAACTCATGTAATAACCAACAAACAAAGCCTAACTTTGTGACCAAAATGTTTAATAA 1733
DB 5197 GAACTCATGTAATAACCAACAAACAAAGCCTAACTTTGTGACCAAAATGTTTAATAA 5256
QY 1734 TTATTTTAAATGATGAATTAATAAGTATATATTTATTTGTTGTTGTTGTTGTTGTT 1793
DB 5257 TTATTTTAAATGATGAATTAATAAGTATATATTTATTTGTTGTTGTTGTTGTTGTT 5316
QY 1794 GAAGTATGTAATGATGAGATGAGCAATGAGCAACCAATTTTATACCTTGTCTGATTA 1853
DB 5317 GAAGTATGTAATGATGAGATGAGCAATGAGCAACCAATTTTATACCTTGTCTGATTA 5376
QY 1854 TTTGCAATTTTAAAAATTTTCTCTCATTTTACCAACCACTGTGCACTGAAGAAATCTTTCAAG 1913
DB 5377 TTTGCAATTTTAAAAATTTTCTCTCATTTTACCAACCACTGTGCACTGAAGAAATCTTTCAAG 5436
QY 1914 GAATAGGCACACTGAGAGTCAAACTGTGCAAGGGGTACTGTGGAAGAAAGCTATTTCAAAA 1973
DB 5437 GAATAGGCACACTGAGAGTCAAACTGTGCAAGGGGTACTGTGGAAGAAAGCTATTTCAAAA 5496

QY 1974 ACTGTCCTTAATAAAGAAATACATTGACGGCCAAAAGTAAGTTACACACATTCATGG 2033
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Db 5497 ACTGTCCCTTAATAAAGAAATACATTGACGGCCAAAAGTAAGTTACACACATTCATGG 5556
QY 2034 AAGCTATATTGTCCTGGCTGTCCTATTTCATGGAATTGACAGTTTCTGTATACCT 2093
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Db 5557 AAGCTATATTGT - CTGGCTGTGCTATTTCATGGAATTGACAGTTTCTGTATACCT 5615
QY 2094 ATTGTCATTTTCTTTTTCACAGAAAAAGTGTGAGAAAGAAAGACGAGAGTAAACCA 2153
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Db 5616 ATTGTCATTTTCTTTTTCACAGAAAAAGTGTGAGAAAGAAAGACGAGAGTAAACCA 5675
QY 2154 TTCCTAGACTACCTGCAAGAGTTTCTGTGTAATGAACACCGAGTGAATATAGAAAGT 2213
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Db 5676 TTCCTAGACTACCTGCAAGAGTTTCTGTGTAATGAACACCGAGTGAATATAGAAAGT 5735
QY 2214 TGAGACTAACTGGTTGTTGTCAGCCAAAGATTGGAGAGAGACATTTTACTGCAG 2273
|||||
Db 5736 TGAGACTAACTGGTTGTTGTCAGCCAAAGATTGGAGAGAGACATTTTACTGCAG 5795
QY 2274 TGAGATGAGGGCCAAAGAGATCAGGCCCTTAATTTCAATATATTAATTAACCTCAGAG 2333
|||||
Db 5796 TGAGATGAGGGCCAAAGAGATCAGGCCCTTAATTTCAATATATTAATTAACCTCAGAG 5855
QY 2334 GAAAGTAAATATTTCAGGCATACTGACACTTTCAGAGAAAGCATAAATCTTAAATAT 2393
|||||
Db 5856 GAAAGTAAATATTTCAGGCATACTGACACTTTCAGAGAAAGCATAAATCTTAAATAT 5915
QY 2394 ATTTCAGATATCAGAAATCATTTGAAGTATTTCTCCAGGCAAAATGATTAATCTTTTC 2453
|||||
Db 5916 ATTTCAGATATCAGAAATCATTTGAAGTATTTCTCCAGGCAAAATGATTAATCTTTTC 5975
QY 2454 TTATTTAATTAACATCTCTGTAATAATGCTGTTAATTAATTAATTAATTAATGTTA 2513
|||||
Db 5976 TTATTTAATTAACATCTCTGTAATAATGCTGTTAATTAATTAATTAATTAATGTTA 6035
QY 2514 AGAATTTGGTAAATAGTATTTATTTAATGTTATGTTGTTCTAATAAACAATAATAG 2573
|||||
Db 6036 AGAATTTGGTAAATAGTATTTATTTAATGTTATGTTGTTCTAATAAACAATAATAG 6095
QY 2574 ACAACTGTCAATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2633
|||||
Db 6096 ACAACTGTCAATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 6153
QY 2634 TGAGTACATGCCCCAGTTTGGAGGAGGGGTGAGCACATGTTGGCTGAGCATCCCATTTTC 2693
|||||
Db 6154 TGAGTACATGCCCCAGTTTGGAGGAGGGGTGAGCACATGTTGGCTGAGCATCCCATTTTC 6213
QY 2694 TCTGGAGAGTCTCAAGGTTGCAAGGACACAGAGGTTGGAAGTATAGCAGACTTA 2753
|||||
Db 6214 TCTGGAGAGTCTCAAGGTTGCAAGGACACAGAGGTTGGAAGTATAGCAGACTTA 6273
QY 2754 GTGGGATGTGGGAGCAGGACACAGAGGTTGAACCTGTTTCTCTCTACAGTA 2813
|||||
Db 6274 GTGGGATGTGGGAGCAGGACACAGAGGTTGAACCTGTTTCTCTCTACAGTA 6333
QY 2814 TATCCAGAACCTGGGATGTCGAAGGTTAAATGTTAGGGAATAAATGAATGATGCTT 2873
|||||
Db 6334 TATCCAGAACCTGGGATGTCGAAGGTTAAATGTTAGGGAATAAATGAATGATGCTT 6392
QY 2874 TCCCAAGA-TGATTTAGAACTAAATGAGTTGTAAG--CTCCCTGGAAGAAGGATGT- 2929
|||||
Db 6393 TCCCAAGACTGATTTAGAACTAAATGAGTTGTAAGGCTCCCTGGAAGAAGGAGCTG 6452
QY 2930 --GGAACCTGTAACTAGGTTCTCTGCCCCAGCTGTGAGAGAAATTTGGCAGATC-ATCTCA 2986
|||||
Db 6453 TGGGAACCTGTAACTAGGTTCTCTGCCCCAGCTGTGAGAGAAATTTGGCAGATCAATCTCA 6512
QY 2987 TTGCCAGTATAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 3044
|||||
Db 6513 TTGCCAGTATAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 6572

QY 3045 CCACCTGACCCTGCACCATACAAAGG-ACAGAGAGACA-TGTAAGGCGAGTCCCATTA 3102
|||||
Db 6573 CCACCTGACCCTGCACCATACAAAGGAGAGAGAGACACTGTAGGCGAGTCCCATTA 6632
QY 3103 GAAAGACTGAGTTCCGTATTCCC-GGGGACAGGGCAGCACCAGCGCCACACACA-TCCATT 3160
|||||
Db 6633 GAAAGACTGAGTTCCGTATTCCCAGGGGACAGGGCAGCACCAGCGCCACACACTCCATT 6692
QY 3161 CTGCTGCTTATGGCTATCAGTACGATCACTAGAGATTCCTGTTGAGAAAACTCTTC 3220
|||||
Db 6693 CTGCTGCTTATGGCTATCAGTACGATCACTAGAGATTCCTGTTGAGAAAACTCTTC 6752

RESULT 5

AAF20978

ID AAF20978 standard; DNA; 3241 BP.

AAF20978;

DT 14-MAR-2001 (first entry)

DE Human low adenosine antisense oligonucleotide related sequence #2545.

XX Low adenosine antisense oligonucleotide; phosphorothioate; allergy;
KW human; airway disorder; bronchoconstriction; lung inflammation;
KW surfactant depletion; respiratory; bronchodilator; antiinflammatory;
KW immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic;
KW respiratory obstruction; pulmonary obstruction; impeded respiration;
KW surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;
KW respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
KW pulmonary hypertension; emphysema; pulmonary transplantation rejection;
KW chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
KW cancer; ss.

OS Homo sapiens.

PN WO200062736-A2.

PD 26-OCT-2000.

PF 24-MAR-2000; 2000WO-US08020.

PR 06-APR-1999; 99US-0127958.

PA (UYEC-) UNIV EAST CAROLINA.

PA (NYCE/) NYCE J W.

PI Nyce JW;

DR WPI; 2000-679539/66.

XX Low adenosine (A) content antisense oligonucleotides which do not
PT trigger adenosine receptors during metabolism, useful e.g. for treating
PT cancers and respiratory obstructions -

PS Disclosure; Page 787-788; 1592pp; English.

XX The present invention describes low adenosine (A) content antisense
CC oligonucleotides and compositions (I) comprising them. In the antisense
CC oligonucleotides the A is replaced by a 'universal' or alternative base.
CC (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,
CC immunosuppressive, antiasthmatic, hypotensive and cytostatic activities.
CC The antisense oligonucleotides and (I) can be used to down-regulate the
CC expression and or activity of target polypeptides associated with
CC lung/respiratory disorders and malignancies, such as stimulating and
CC activating peptide factors and transmitters, transcription factors,
CC immunoglobulins and antibodies, antibody receptors, cytokines and
CC chemokines, endogenously produced specific and non-specific enzymes,
CC binding proteins, adhesion molecules and their receptors, cytokine and
CC chemokine receptors, adenosine receptors, bradykinin receptors, central
CC nervous system (CNS) and peripheral nervous and non-nervous system
CC receptors, CNS and peripheral nervous and non-nervous system peptide
CC transmitters, defensins, growth factors, vasoactive peptides and

CC receptors, binding proteins and malignancy associated proteins. The
 CC antisense oligonucleotides may be used in this way to treat disorders
 CC including respiratory obstruction (especially pulmonary obstruction
 CC and/or bronchoconstriction) and/or lung inflammation, allergy(ies)
 CC and/or surfactant hypoproduction which are associated with a disease or
 CC condition selected from pulmonary vasocostriction, inflammation,
 CC allergies, asthma, impeded respiration, respiratory distress syndrome
 CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
 CC hypertension, emphysema, chronic obstructive pulmonary disease (COPD),
 CC pulmonary transplantation rejection, pulmonary infections, bronchitis,
 CC and/or cancer. AAF18434 to AAF21543 represent human polynucleotide
 CC fragments and antisense oligonucleotides used in the exemplification of
 CC the present invention.

xx Sequence 3241 BP; 1026 A; 546 C; 632 G; 1037 T; 0 other;

Query Match 91.0%; Score 2940; DB 21; Length 3241;

Best Local Similarity 98.5%; Pred. No. 0;

Matches 3191; Conservative 0; Mismatches 20; Indels 29; Gaps 21;

QY 1 ATCCTAATCAAGACCCAGTGAACAGACTGACCCCTGCCAAGCTTGCA-TTTCAT 59
 Db 3 ATCCTAATCAAGACCCAGTGAACAGACTGACCCCTGCCAAGCTTGCAATT 62
 QY 60 TCAATCAGTCTTCCACACAGATTTTCAATTTCTTTAAGACAGATTAATCTAGCCAC 119
 Db 63 TCAATCAGTCTTCCACACAGATTTTCAATTTCTTTAAGACAGATTAATCTAGCCAC 122
 QY 120 AGTCATAGTAGACATAGCCGATCTTGAAAAAACAATCCCAATATTATGTATTTAG 179
 Db 123 AGTCATAGTAGACATAGCCGATCT--GAAAAAACAATCCCAATATTATGTATTTAG 180
 QY 180 CATAAATTCGTCTTGTAGTGTCTACCTTACTTTGTTTGCACACATCTTTAAGAGCA 239
 Db 181 CATAAATTCGTCTTGTAGTGTCTACCTTACTTTGTTTGCACACATCTTTAAGAGCA 240
 QY 240 AGTTAATTTCTGATTTTAAGAAATGCAAAATGTGGGCAATGATTTAACCCAAAGAT 299
 Db 241 AGTTAATTTCTGATTTTAAGAAATGCAAAATGTGGGCAATGATTTAACCCAAAGAT 300
 QY 300 TCCTCCGTAATAGAAATGTTTAAAGGGGGGAAACAGGATTTTATTATAAAGA 359
 Db 301 TC-TTCGTAATAGAAATGTTTAAAGGGGGGAAACAGGATTTTATTATAAAGA 358
 QY 360 TAAAGTAAATTTATTTTAAAGATTAAGCATTTGAAACATTTAGTTACGATATGC 419
 Db 359 TAAAGTAAATTTATTTTAAAGATTAAGCATTTGAAACATTTAGTTACGATATGC 418
 QY 420 CATATTAGGCATCTCTATCTGATGTTAGAAATTTATTCATTCCTCAAGACAGACAA 479
 Db 419 CATATTAGGCATCTCTATCTGATGTTAGAAATTTATTCATTCCTCAAGACAGACAA 478
 QY 480 TAAATTGACTGGGAGCGAGCTTGTACTATGCACTTCTTGGCAAAAGCAACGACAGA 539
 Db 479 TAAATTGACTGGGAGCGAGCTTGTACTATGCACTTCTTGGCAAAAGCAACGACAGA 538
 QY 540 ACGTTTACAGCCATGAGGATGCTTGTGCAATTTGAGTTGCTAGCTTTGGAGCTGCCTA 599
 Db 539 ACGTTTACAGCCATGAGGATGCTTGTGCAATTTGAGTTGCTAGCTTTGGAGCTGCCTA 598
 QY 600 CGTGTATGCCATCCACAGAAATTCACCAAGTGCATTTGGTGAAGAGACCTTGGCACT 659
 Db 599 CGTGTATGCCATCCACAGAAATTCACCAAGTGCATTTGGTGAAGAGACCTTGGCACT 658
 QY 660 GCTTCTACTCAGCACTGCTGTGATGCAATGAGTAATTTCTTATGATTTCCCTAC 719
 Db 659 GCTTCTACTCAGCACTGCTGTGATGCAATGAGTAATTTCTTATGATTTCCCTAC 718
 QY 720 AGTCTGTAAGTCATAGTAATCATTTGTGATGTTCCCTTACTATATATAGAGATCTG 779
 Db 719 AGTCTGTAAGTCATAGTAATCATTTGTGATGTTCCCTTACTATATATAGAGATCTG 778
 QY 780 TTATAAATAATAGATTTCTGAGCACATTTAGTACATGGGTGATTAATACTACACAGCAAA 839

Db 779 TTATAAATAATAGATTTCTGAGCACATTTAGTACATGGGTGATTAATACTACACAGCAAA 838
 QY 840 CATCTGTAAAGTTATGAATGCTGTGCTGTGTAATAATGATTTCTTCTCCTC 899
 Db 839 CATCTGTAAAGTTATGAATGCTGTGCTGTGTAATAATGATTTCTTCTCCTC 898
 QY 900 TCCAGACTGTGAGGATTCCTGTCTGTGATCAATAAATGTAAGTTAATGATTCAGT 959
 Db 899 TCCAGACTGTGAGGATTCCTGTCTGTGATCAATAAATGTAAGTTAATGATTCAGT 958
 QY 960 AAAATGATGGCATGAATAAGTAATTTCTGTTTAAAGCTGTAATCATTTAGTATCAT 1019
 Db 959 AAAATGATGGCATGAATAAGTAATTTCTGTTTAAAGCTGTAATCATTTAGTATCAT 1018
 QY 1020 GGAACATTTAATTTCTATATTTTGTTCATATGAGGTGCTGTAATGCTGACTTA 1079
 Db 1019 GGAACATTTAATTTCTATATTTTGTTCATATGAGGTGCTGTAATGCTGACTTA 1078
 QY 1080 TAAATATGAGGAATGCTTTTATCAAGTAGAATCCTTTAACAAGTGATTTAGGCTCTT 1139
 Db 1079 TAAATATGAGGAATGCTTTTATCAAGTAGAATCCTTTAACAAGTGATTTAGGCTCTT 1138
 QY 1140 TGGTATGTTGTTAGTTTCCCTTCCCAAGACATGCTGTCA-GGATTCCTTCCAGAGG 1198
 Db 1139 TGGTATGTTGTTAGTTTCCCTTCCCAAGACATGCTGTCAAGGATTCCTTCCAGAGG 1197
 QY 1199 ATTCACACATGAGTGAGAGGTGCGTGTAGTCTCCGTGACATGCTGCTCTCTACATC 1258
 Db 1198 ATTCACACATGAGTGAGAGGTGCGTGTAGTCTCCGTGACATGCTGCTCTCTACATC 1257
 QY 1259 TAAAGTGTTCGAAAGTATTAGCAACTCAGAAATTTATTTTGAACCATGATCAGTAG 1318
 Db 1258 TAAAGTGTTCGAAAGTATTAGCAACTCAGAAATTTATTTTGAACCATGATCAGTAG 1317
 QY 1319 ACATTAATAATATATCAAAATGCCCTATATTAATAA-TTCTGATCTTAAATAATATAG 1377
 Db 1318 ACATTAATAATATATCAAAATGCCCTATATTAATAA-TTCTGATCTTAAATAATATAG 1377
 QY 1378 ACTATATGATGTTG-TGATGCAAT--GAATATGCTGTGATATTAATAATATAT 1434
 Db 1378 ACTATATGATGTTGTTGATGCAATTTGAATATGCTGTGATATTAATAATATAT 1437
 QY 1435 ATAG-TTTATTTAGTCAAAATAGAAATTAACACTACAGCTAGAACTGTGAAACACATGTAT 1493
 Db 1438 ATAGTTTATTTAGTCAAAATAGAAATTAACACTACAGCTAGAACTGTGAAACACATGTAT 1497
 QY 1494 ATGAGTTTAATGTATTAATGCAATTTACACTTCCAAACATTTTTCAGTTACATATTA 1553
 Db 1498 ATGAGTTTAATGTATTAATGCAATTTACACTTCCAAACATTTTTCAGTTACATATTA 1557
 QY 1554 GTTATATCTTTAATAAACTCCTCAGTAATCATATAAGCTTCATCTACTTTTGAATAAT 1613
 Db 1558 GTTATATCTTTAATAAACTCCTCAGTAATCATATAAGCTTCATCTACTTTTGAATAAT 1617
 QY 1614 TTATCTTAATATGTTGTTGTTGCTAGAAAAACAACAACAAAAAAGCTTTGGAGAAGG 1673
 Db 1618 TTATCTTAATATGTTGTTGTTGCTAGAAAAACAACAACAAAAAAGCTTTGGAGAAGG 1677
 QY 1674 GAACATCATGTAATATACCAAAACAAAGCCTAATCTTGTGACCAAAATGTTTAATAA 1733
 Db 1678 GAACATCATGTAATATACCAAAACAAAGCCTAATCTTGTGACCAAAATGTTTAATAA 1737
 QY 1734 TTATTTTAAATTGATGAATTTAAAGATATATATTTATTTGTGTGATATATGATGTTT 1793
 Db 1738 TTATTTTAAATTGATGAATTTAAAGATATATATTTATTTGTGTGATATATGATGTTT 1797
 QY 1794 GAAGTATGTATACATTCAGAAATGGAATGGAACCAATTTTATACCTTGTCTGATTA 1853
 Db 1798 GAAGTATGTATACATTCAGAAATGGAATGGAACCAATTTTATACCTTGTCTGATTA 1857
 QY 1854 TTTCATTTTAAAAATTTTCTCATTTAGCAACCACTGTGACATGAAGAAATCTTTCAGG 1913

Db 1858 TTTCATTTTAAAAATTTCTCATTAGCACCAACTGTGCACACTGAAGAAATCTTTCAGG 1917

QY 1914 GAATAGGCACACTGAGAGTCAAACTGTGCAAGGGGTACTGTGAAAGACTATTCAAAA 1973

Db 1918 GAATAGGCACACTGAGAGTCAAACTGTGCAAGGGGTACTGTGAAAGACTATTCAAAA 1977

QY 1974 ACTTGCTCTTAATAAGAAATACATTGACGGGCCAAAAAGTAAGTTACACACTTCAATGG 2033

Db 1978 ACTTGCTCTTAATAAGAAATACATTGACGGGCCAAAAAGTAAGTTACACACTTCAATGG 2037

QY 2034 AAGCTATATTGCTGCTGCTGCTGCTATTTCTATGGAATTGACAGTTTCTGTAATACCT 2093

Db 2038 AAGCTATATTGCTGCTGCTGCTGCTATTTCTATGGAATTGACAGTTTCTGTAATACCT 2096

QY 2094 ATTGTCATTTTCTTTTTCACAGAAAAAGTGTGAGAAAGAAAGACGAGAGTAAACCA 2153

Db 2097 ATTGTCATTTTCTTTTTCACAGAAAAAGTGTGAGAAAGAAAGACGAGAGTAAACCA 2156

QY 2154 TTCTAGACTACCTGCAAGAGTTTCTGCTGTAATGAACACCGAGTGAATAGAAAGT 2213

Db 2157 TTCTAGACTACCTGCAAGAGTTTCTGCTGTAATGAACACCGAGTGAATAGAAAGT 2216

QY 2214 TGAGACTAAACTGGTTGTGTCAGCCAAAGATTTTGAGAGAGAGACATTTTACTGCAG 2273

Db 2217 TGAGACTAAACTGGTTGTGTCAGCCAAAGATTTTGAGAGAGAGACATTTTACTGCAG 2276

QY 2274 TGAGAAATGAGGGCCAGAAAGAGTCAAGCCCTTAATTTCAATATTAATTAACCTCAGAG 2333

Db 2277 TGAGAAATGAGGGCCAGAAAGAGTCAAGCCCTTAATTTCAATATTAATTAACCTCAGAG 2336

QY 2334 GAAAGTAAATATTTCAAGGCATCTGACACTTTCAGAGAAAGCATAAATTTCTAAATAT 2393

Db 2337 GAAAGTAAATATTTCAAGGCATCTGACACTTTCAGAGAAAGCATAAATTTCTAAATAT 2396

QY 2394 ATTTGAGATATCAGAAATCATTTGAAGTATTTCTCCAGGCAAAATTTGATATCTTTTTC 2453

Db 2397 ATTTGAGATATCAGAAATCATTTGAAGTATTTCTCCAGGCAAAATTTGATATCTTTTTC 2456

QY 2454 TTATTTAATTAACATCTCTGTAATAATGCTGTAACCTTAATAGTATTAATGAATGTTA 2513

Db 2457 TTATTTAATTAACATCTCTGTAATAATGCTGTAACCTTAATAGTATTAATGAATGTTA 2516

QY 2514 AGAATTTGGTAAATAGTATTTAATTAATGTTGTGTCTTAATTAACAAACAAATAG 2573

Db 2517 AGAATTTGGTAAATAGTATTTAATTAATGTTGTGTCTTAATTAACAAACAAATAG 2576

QY 2574 ACAACTGTTCATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2633

Db 2577 ACAACTGTTCATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2634

QY 2634 TGAGTACATGCCCCAGTTTGAGAGAGGGGTGAGCACATGTGGCTGAGCATCCCATTTTC 2693

Db 2635 TGAGTACATGCCCCAGTTTGAGAGAGGGGTGAGCACATGTGGCTGAGCATCCCATTTTC 2694

QY 2694 TCTGAGAGAGTCTCAAGGTTGCAAGGCACACAGAGGTGGAAGTGAATCTAGCAGACTTA 2753

Db 2695 TCTGAGAGAGTCTCAAGGTTGCAAGGCACACAGAGGTGGAAGTGAATCTAGCAGACTTA 2754

QY 2754 GTGGGATGTGGGAGCAGGAGCACAGGAGAGGTGAACCTGTTTCTCTACAGTA 2813

Db 2755 GTGGGATGTGGGAGCAGGAGCACAGGAGAGGTGAACCTGTTTCTCTACAGTA 2814

QY 2814 TATCCAGAACCTGGGATGGTGAAGGTAATGGTAGGAATAATGAATGATGTGCTT 2873

Db 2815 TATCCAGAACCTGGGATGGTGAAGGTAATGGTAGGAATAATGAATGATGTGCTT 2873

QY 2874 TCCCAAGA-TGATTTGAGAACTAAATGAGTTGTAAG--CTCCCTGAGAGAGGAGTGT- 2929

Db 2874 TCCCAAGACTGATTTGAGAACTAAATGAGTTGTAAGGCTCCCTGAGAGAGGAGTGT 2933

QY 2930 --GGAACCTGTACTAGGTTCTCTGCCCCAGCTGTGAGAGAAATTTGGCAGATC-ATCTCA 2986

Db 2934 TGGGAACCTGTACTAGGTTCTCTGCCCCAGCTGTGAGAGAAATTTGGCAGATCAATCTCA 2993

QY 2987 TTGCCAGTATAGAGAGGAGGAGCCAGAAACCTCTCTGCCAAGGCTGCAGGGTCTTA-- 3044

Db 2994 TTGCCAGTATAGAGAGGAGGAGCCAGAAACCTCTCTGCCAAGGCTGCAGGGTCTTA-- 3053

QY 3045 CCACCTGACCTGCACCATTAACAAAGG-ACAGAGAGACA-TGCTAGGGCAGTCCCATTA 3102

Db 3054 CCACCTGACCTGCACCATTAACAAAGGAGAGAGAGACTGCTAGGGCAGTCCCATTA 3113

QY 3103 GAAAGACTGAGTTCCTGATTTCC-GGGGCAGGGCAGCAGCAGCCGACACACA-TCCATT 3160

Db 3114 GAAAGACTGAGTTCCTGATTTCCCGGGGGCAGGGCAGCAGCAGCCGACACACTTCATT 3173

QY 3161 CTGCTGCTTATGCTATCAGTACATCAGATTCCTGTTGAGAAAACTTCTC 3220

Db 3174 CTGCTGCTTATGCTATCAGTACATCAGATTCCTGTTGAGAAAACTTCTC 3233

RESULT 6
AAA34856
ID AAA34856 standard; DNA; 3241 BP.
XX
AC AAA34856;
XX
DT 28-JUL-2000 (first entry)
XX
DE Human adenosine receptor related polynucleotide SEQ ID NO:2545.
XX
KW Human; adenosine receptor; low adenosine antisense oligonucleotide;
KW phosphorothioate; impaired respiration; inflammation; allergy;
KW allergic disease; bronchoconstriction; inhibitor; antiinflammatory;
KW antiallergic; antiasthmatic; cyostatic; analgesic; impaired airway;
KW lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;
KW respiratory distress syndrome; pain; cystic fibrosis; emphysema;
KW pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
KW cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.
XX
OS Homo sapiens.
XX
PN WO200009525-A2.
XX
PD 24-FEB-2000.
XX
PF 03-AUG-1999; 99WO-US17712.
XX
PR 03-AUG-1998; 98US-0095212.
PA (UYEC-) UNIV EAST CAROLINA.
XX
PI Nyce JW;
XX
DR WPI: 2000-205971/18.
XX
PT New antisense oligonucleotides useful for treating e.g. pulmonary
PT vasoconstriction, inflammation, allergies, asthma, hypertension,
PT bronchitis, emphysema, respiratory distress syndrome, ischemia or
PT cancers
XX
PS Disclosure: Page 715-716; 1343pp; English.
XX
CC The present invention describes a new composition comprising an
CC antisense oligonucleotide (ON) with low adenosine (up to 15%), which
CC targets nucleic acids involved in bronchoconstriction, allergies, and/or
CC inflammation. The ON can have antiinflammatory, antiallergic,
CC antiasthmatic, cyostatic and analgesic activities. The compositions are
CC useful for the treatment of diseases associated with inflammation,
CC impaired airways, including lung disease and diseases whose secondary
CC effects afflict the lungs of a subject. They can be used for treating
CC e.g. ischaemic conditions, pulmonary vasoconstriction, allergies,
CC asthma, impaired respiration, respiratory distress syndrome, pain, cystic
CC fibrosis, pulmonary hypertension, emphysema, chronic obstructive
CC pulmonary disease (COPD), and cancers such as leukaemias, lymphomas,
CC carcinomas, and cancers which may metastasise to the lungs, including

QY	1914	GAATAGGCACACTGGAGAGTCAAACTGTGCAAGGGGGTACTGTGMAAGACTATTCAAAA	1973
Db	1918	GAATAGGCACACTGGAGAGTCAAACTGTGCAAGGGGGTACTGTGMAAGACTATTCAAAA	1977
QY	1974	ACTTGCTCTTAATAAAGAAATACATTGACGGCCAAAAAGTAAGTTACACACATTCAAATGC	2033
Db	1978	ACTTGCTCTTAATAAAGAAATACATTGACGGCCAAAAAGTAAGTTACACACATTCAAATGC	2037
QY	2034	AAGCTATATTTGTCTGGCTGTGCCCTATTTCTATGGAATTGACAGTTTCCGTGAATACCT	2093
Db	2038	AAGCTATATTTGT - CTGGCTGTGCCCTATTTCTATGGAATTGACAGTTTCCGTGAATACCT	2096
QY	2094	ATTGTCATTTTCTTTTTCACAGAAAAAGTGTGAGAGAAAGACGAGAGTAACCAA	2153
Db	2097	ATTGTCATTTTCTTTTTCACAGAAAAAGTGTGAGAGAAAGACGAGAGTAACCAA	2156
QY	2154	TTCCTAGACTACCTGCAAGAGTTTCTTGTTATTAACAACCGAGTGATATAGAAAGT	2213
Db	2157	TTCCTAGACTACCTGCAAGAGTTTCTTGTTATTAACAACCGAGTGATATAGAAAGT	2216
QY	2214	TGAGACTAAACTGGTTGTGTTCACAGCCAAAGATTTTGAGAGGAGAGACATTTTACTGCAG	2273
Db	2217	TGAGACTAAACTGGTTGTGTTCACAGCCAAAGATTTTGAGAGGAGAGACATTTTACTGCAG	2276
QY	2274	TGAGAAATGAGGGCCCAAGAAAGAGTCAGGCCCTTAATTTTCAATATATTAATTTAACTCAGAG	2333
Db	2277	TGAGAAATGAGGGCCCAAGAAAGAGTCAGGCCCTTAATTTTCAATATATTAATTTAACTCAGAG	2336
QY	2334	GAAAGTAAATATTTTCAGGCATACTGACACCTTTGCCAGAAAAACATAAAAATTCCTAAAAATAT	2393
Db	2337	GAAAGTAAATATTTTCAGGCATACTGACACCTTTGCCAGAAAAACATAAAAATTCCTAAAAATAT	2396
QY	2394	ATTTTCAGATATCAGAAATCATTGAAGTATTTTCCTCCAGGCCAAAAATGATATATACCTTTTTC	2453
Db	2397	ATTTTCAGATATCAGAAATCATTGAAGTATTTTCCTCCAGGCCAAAAATGATATATACCTTTTTC	2456
QY	2454	TTATTTAACTTAACTCTGTAAAAATGTCGTGTTAACTTAATAGTATTTATGAAGTGTTA	2513
Db	2457	TTATTTAACTTAACTCTGTAAAAATGTCGTGTTAACTTAATAGTATTTATGAAGTGTTA	2516
QY	2514	AGAAATTTGGTAAATTAAGTATTTATTTAATGTTATGTGTCTAATAAAAACAAAAATAG	2573
Db	2517	AGAAATTTGGTAAATTAAGTATTTATTTAATGTTATGTGTCTAATAAAAACAAAAATAG	2576
QY	2574	ACAACCTGTTCAATTTGCTGCTGGCCCTCTGTCCCTTACCAATTTGAAGTTAGCACAGTCCAT	2633
Db	2577	ACAACCTGTTCAATTTGCTGCTGGCCCTCTGTCTGTC - TTAGCAATTTGAAGTTAGCACAGTCCAT	2634
QY	2634	TGAGTACATGCCCCAGTTTGGAGGAAGGGCTGTGAGACATGTGGCTGAGCATCCCATTTTC	2693
Db	2635	TGAGTACATGCCCCAGTTTGGAGGAAGGGCTGTGAGACATGTGGCTGAGCATCCCATTTTC	2694
QY	2694	TCTGGAGAAAGTCTCAAGGTTGCCAAGGCACACACAGAGGTGGAAGTGAATCTAGCAGACTTA	2753
Db	2695	TCTGGAGAAAGTCTCAAGGTTGCCAAGGCACACACAGAGGTGGAAGTGAATCTAGCAGACTTA	2754
QY	2754	GTCGGGATGTGGGGACAGGGACACAGGCAGAGGTGAACCTGGTTTTCTCTACAGTA	2813
Db	2755	GTCGGGATGTGGGGACAGGGACACAGGCAGAGGTGAACCTGGTTTTCTCTACAGTA	2814
QY	2814	TATCCAGAAACCTGGGATGGCTCGAAGGGTAAATGGTAGGGAATAAATGAATGAATGTCGTT	2873
Db	2815	TATCCAGAAACCTGGGATGGCT - GCAGGGTAAATGGTAGGGAATAAATGAATGAATGTCGTT	2873
QY	2874	TCCCAAGA - TGATTTGTAGAACTAAAAATGAGTTGTAG - -CTCCCTGGAAGAGGATGT -	2929
Db	2874	TCCCAAGACTGATTTGTAGAACTAAAAATGAGTTGTAGAGCCCTCCCTGGAAGAGGAGTGT	2933
QY	2930	--GGAACCTGTAAGTTCCTGCCCCAGCCGTGTGAGAAAGAAATTTGGCAGATC - ATCTCA	2986
Db	2934	TGGGAACCTGTAAGTTCCTGCCCCAGCCGTGTGAGAAAGAAATTTGGCAGATCAATCTCA	2993

[illegible]

RESULT 7
AAF20980
ID AAF20980 standard; DNA; 4057 BP.

DT 14-MAR-2001 (first entry)

DE Human low adenosine antisense oligonucleotide related sequence #2547.

KW Low adenosine antisense oligonucleotide; phosphorothioate; allergy;
KW human; airway disorder; bronchoconstriction; lung inflammation;
KW surfactant depletion; respiratory; bronchodilator; antiinflammatory;
KW immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic;
KW respiratory obstruction; pulmonary obstruction; impeded respiration;
KW surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;
KW respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
KW pulmonary hypertension; emphysema; pulmonary transplantation rejection;
KW chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
KW cancer; ss.

Os Homo sapiens.

PN WO200062736-A2.

PD 26-OCT-2000.

PF 24-MAR-2000; 2000WO-US08020.

PR 06-APR-1999; 99US-0127958.

PA (UYEC-) UNIV EAST CAROLINA

XX

XXXX

XX

PT trigger adenosine receptors during metabolism, useful e.g. for treating

xx

1. **XX**
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 91. **XX**
 92. **XX**
 93. **XX**
 94. **XX**
 95. **XX**
 96. **XX**
 97. **XX**
 98. **XX**
 99. **XX**
 100. **XX**

oligonucleotides and compositions (I) comprising them. In the antisense

(I) can have respiratory, bronchodilator, antiinflammatory, analgesic,

CC The antisense oligonucleotides and (I) can be used to down-regulate the

lung/respiratory disorders and malignancies, such as stimulating and

CC immunoglobulins and antibodies, antibody receptors, cytokines and

CC binding proteins, adhesion molecules and their receptors, cytokine and

Db 1798 GAAGTATGTATACATTGCAGAAATGACAAATGACCAAAATTTTATACCTTGTCTTGATTA 1857
QY 1854 TTTCATTTTAAAAATTTCTCATTTTAGCACCACTGTGCACCTGAAGAAATCTTTCAGG 1913
Db 1858 TTTCATTTTAAAAATTTCTCATTTTAGCACCACTGTGCACCTGAAGAAATCTTTCAGG 1917
QY 1914 GAATAGGCACACTGAGAGTCAAACTGTGCAGAGGGGTACTGTGGAAGACTATTCAAA 1973
Db 1918 GAATAGGCACACTGAGAGTCAAACTGTGCAGAGGGGTACTGTGGAAGACTATTCAAA 1977
QY 1974 ACTTGCTCTTAATAAAGAAATACATTGACGGCCCAAAAAGTAACTACACATTCATGG 2033
Db 1978 ACTTGCTCTTAATAAAGAAATACATTGACGGCCCAAAAAGTAACTACACATTCATGG 2037
QY 2034 AAGCTATATTTGCTGCGCTGTGCTATTTTATGGAATTGACAGTTTCTGTATACCT 2093
Db 2038 AAGCTATATTTGCTGCGCTGTGCTATTTTATGGAATTGACAGTTTCTGTATACCT 2096
QY 2094 ATTGTCATTTTCTTTTTCACAGAAAAAGTGTGAGAGAAAGAGAGAGTAAACCA 2153
Db 2097 ATTGTCATTTTCTTTTTCACAGAAAAAGTGTGAGAGAAAGAGAGTAAACCA 2156
QY 2154 TTCTAGACTACCTGCAAGAGTTTCTTGCTATGACACACCGAGTGAATAGAAAGT 2213
Db 2157 TTCTAGACTACCTGCAAGAGTTTCTTGCTATGACACACCGAGTGAATAGAAAGT 2216
QY 2214 TGAGACTAACTGTTTGTTCACAGCCCAAGATTTTGAGAGAGAGACATTTTACTGCAG 2273
Db 2217 TGAGACTAACTGTTTGTTCACAGCCCAAGATTTTGAGAGAGAGACATTTTACTGCAG 2276
QY 2274 TGAGAAATGAGGGCCCAAGAAAGAGTCAAGGCCCTTAATTTCAATATATTAACCTCAGAGG 2333
Db 2277 TGAGAAATGAGGGCCCAAGAAAGAGTCAAGGCCCTTAATTTCAATATATTAACCTCAGAGG 2336
QY 2334 GAAAGTAAATATTTTCAGGCATCTGACACCTTTCAGAGAAAGCATAAATCTTAAATAT 2393
Db 2337 GAAAGTAAATATTTTCAGGCATCTGACACCTTTCAGAGAAAGCATAAATCTTAAATAT 2396
QY 2394 ATTTCAGATATCAGAAATCATTTGAAGTATTTCTCCAGGCAAAATGATATACTTTTTC 2453
Db 2397 ATTTCAGATATCAGAAATCATTTGAAGTATTTCTCCAGGCAAAATGATATACTTTTTC 2456
QY 2454 TTATTTAATTAACATCTCTGTAATAATGCTGTAACTTAATAGTATTTGAATGTTA 2513
Db 2457 TTATTTAATTAACATCTCTGTAATAATGCTGTAACTTAATAGTATTTGAATGTTA 2516
QY 2514 AGAATTTGTAATATAGTATTTTAAATGTAATGTTGTTCTTAATAAACAATAATAG 2573
Db 2517 AGAATTTGTAATATAGTATTTTAAATGTAATGTTGTTCTTAATAAACAATAATAG 2576
QY 2574 ACAACTGTCAATTTGCTGCTGCGCTGTCTTACCAATTTGAAGTTAGCACAGTCCAT 2633
Db 2577 ACAACTGTCAATTTGCTGCTGCGCTGTCTTACCAATTTGAAGTTAGCACAGTCCAT 2634
QY 2634 TGAGTACATGCCAGTTTGAGAGAGGGTCTGAGCACATGTGGCTGAGCATCCCATTTTC 2693
Db 2635 TGAGTACATGCCAGTTTGAGAGAGGGTCTGAGCACATGTGGCTGAGCATCCCATTTTC 2694
QY 2694 TCTGAGAGAGTCTCAAGGTTGCAAGGCACACAGAGGTGGAAGTATAGCAGACTTA 2753
Db 2695 TCTGAGAGAGTCTCAAGGTTGCAAGGCACACAGAGGTGGAAGTATAGCAGACTTA 2754
QY 2754 GTGGGATGTGGGAGCAGGAGACACAGCAGAGAGGTGAACCTGTTTCTCTACAGTA 2813
Db 2755 GTGGGATGTGGGAGCAGGAGACACAGCAGAGAGGTGAACCTGTTTCTCTACAGTA 2814
QY 2814 TATCCAGAACCTGGGATGCTGCAAGGTAATGTAAGGAATTAATGAATGATGCTT 2873
Db 2815 TATCCAGAACCTGGGATGCTGCAAGGTAATGTAAGGAATTAATGAATGATGCTT 2873
QY 2874 TCCAAGA-TGATTTAGAACTAAATGAGTTGTAAG--CTCCCTGGAAGAGGAGTGT- 2929
Db 2874 TCCAAGACTGATTTAGAACTAAATGAGTTGTAAGGCGTCCCTGGAAGAGGAGGAGTGT 2933

QY 2930 --GGAACCTGTAAGTGTCTGCCCCAGCCTGTGAGAGAAATTTGGCAGATC-ATCTCA 2986
Db 2934 TGGGAACCTGTAAGTGTCTGCCCCAGCCTGTGAGAGAAATTTGGCAGATCAATCTCA 2993
QY 2987 TTGCCAGTATAGAGAGGAAGCCAGAAACCTCTCTGCAAGAGCCTGCAGGGTCTTAA-- 3044
Db 2994 TTGCCAGTATAGAGAGGAAGCCAGAAACCTCTCTGCAAGAGCCTGCAGGGTCTTAA-- 3053
QY 3045 CCACCTGACCCCTGCACCATAACAAAGG-ACAGAGAGACA-TGGTAGGGCAGTCCCATTA 3102
Db 3054 CCACCTGACCCCTGCACCATAACAAAGGAACAGAGAGACACTGTTAGGGCAGTCCCATTA 3113
QY 3103 GAAAGACTGAGTTCCTGATTTCC--GGGGCAGGGGACAGCAGCCGACACACA-TCCATTT 3160
Db 3114 GAAAGACTGAGTTCCTGATTTCC--GGGGGAGGGGACAGCAGCCGACACACTTCATTT 3173
QY 3161 CTGCCCTGCTTATGCTATCAGTACATCACTAGAGATTTCTGTTGAGAAAACTTCTC 3220
Db 3174 CTGCCCTGCTTATGCTATCAGTACATCACTAGAGATTTCTGTTGAGAAAACTTCTC 3233

RESULT 8

AAA34858

ID AAA34858 standard; DNA; 4057 BP.

XX AAA34858;

AC AAA34858;

XX AAA34858;

DT 28-JUL-2000 (first entry)

XX Human adenosine receptor related polynucleotide SEQ ID NO:2547.

XX Human; adenosine receptor; low adenosine antisense oligonucleotide;
KW phosphorothioate; impaired respiration; inflammation; allergy;
KW allergic disease; bronchoconstriction; inhibitor; antinflammatory;
KW antiallergic; antiasthmatic; cytostatic; analgesic; impaired airway;
KW lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;
KW respiratory distress syndrome; pain; cystic fibrosis; emphysema;
KW pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
KW cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.

XX Homo sapiens.

XX W0200009525-A2.

XX 24-FEB-2000.

XX PD 03-AUG-1999; 99WO-US17712.

XX PR 03-AUG-1998; 98US-0095212.

XX PA (UYEC-) UNIV EAST CAROLINA.

XX PI Nyce JW;

XX DR WPI; 2000-205971/18.

XX New antisense oligonucleotides useful for treating e.g. pulmonary
PT vasoconstriction, inflammation, allergies, asthma, hypertension,
PT bronchitis, emphysema, respiratory distress syndrome, ischemia or
PT cancers

XX Disclosure; Page 717-718; 1343pp; English.

XX The present invention describes a new composition comprising an
CC antisense oligonucleotide (ON) with low adenosine (up to 15%), which
CC targets nucleic acids involved in bronchoconstriction, allergies, and/or
CC inflammation. The ON can have antinflammatory, antiallergic,
CC antiasthmatic, cytostatic and analgesic activities. The compositions are
CC useful for the treatment of diseases associated with inflammation,
CC impaired airways, including lung disease and diseases whose secondary
CC effects afflict the lungs of a subject. They can be used for treating
CC e.g. ischaemic conditions, pulmonary vasoconstriction, allergies,

CC asthma, impeded respiration, respiratory distress syndrome, pain, cystic
CC fibrosis, pulmonary hypertension, emphysema, chronic obstructive
CC pulmonary disease (COPD), and cancers such as leukemias, lymphomas,
CC carcinomas, and cancers which may metastasize to the lungs, including
CC breast and prostate cancer. The reduction of the adenosine content of
CC the ONS reduces side effects. The A-containing ONS break down with the
CC release of deoxyadenosine which activates adenosine receptors causing the
CC bronchoconstriction and inflammation. AAA32313 to AAA35312 represent the
CC nucleotide sequences given in the sequence listing from the present
CC invention, which correspond to SEQ ID NO:1 to 2815, and then the last
CC 185 sequences are also called SEQ ID NO:1 to 185, but the sequences
CC differ from the previously named sequences. SEQ ID NO:11 to 1680
CC (AAA32323 to AAA33992) are specifically claimed ONS from the present
CC invention. N.B. Sequences given in the disclosure of the present
CC invention do not match up with their corresponding SEQ ID NO: sequences
CC given in the sequence listing.

XX Sequence 4057 BP; 1303 A; 683 C; 796 G; 1275 T; 0 other;

Query Match 91.0%; Score 2940; DB 21; Length 4057;
Best Local Similarity 98.5%; Pred. No. 0;
Matches 3191; Conservative 0; Mismatches 20; Indels 29; Gaps 21;

QY 1 ATCCTAATCAGACCCAGTAGACAGAACTCGACCTGCCAAGCTTGCA-TTCCATT 59
Db 3 ATCCTAATCAGACCCAGTAGACAGAACTCGACCTGCCAAGCTTGCA-TTCCATT 62
QY 60 TCAATCACTGCTTCCACACAGATTTTCAATTCTTTAAGACAGATTAATCTAGCCAC 119
Db 63 TCAATCACTGCTTCCACACAGATTTTCAATTCTTTAAGACAGATTAATCTAGCCAC 122
QY 120 AGTCATAGTAGACATAGCCGATCTTGAATAAACATTCCTAATTATGATTTAG 179
Db 123 AGTCATAGTAGACATAGCCGATCTTGAATAAACATTCCTAATTATGATTTAG 180
QY 180 CATAAATCTGTTAGTGTCTACCTTACTTTGTTGACACATCTTTAAGAGA 239
Db 181 CATAAATCTGTTAGTGTCTACCTTACTTTGTTGACACATCTTTAAGAGA 240
QY 240 AGTTAATTTCTGATTTTAAAGAAATGTTGGGCAATGATTAACCCAAAGAT 299
Db 241 AGTTAATTTCTGATTTTAAAGAAATGTTGGGCAATGATTAACCCAAAGAT 300
QY 300 TCCTCCGTAATAGAAATGTTTAAAGGGGGAACAGGATTTTATTAAGAGA 359
Db 301 TC-TTCGTAATAGAAATGTTTAAAGGGGGAACAGGATTTTATTAAGAGA 358
QY 360 TAAAGTAATTTATTTTAAAGATTAAGGCAATTGGAACATTTAGTTACGATATGC 419
Db 359 TAAAGTAATTTATTTTAAAGATTAAGGCAATTGGAACATTTAGTTACGATATGC 418
QY 420 CATATTAGGCAATCTCTATCTGATGTTAGAAATTAATTCATTTCTCAAGACAGACA 479
Db 419 CATATTAGGCAATCTCTATCTGATGTTAGAAATTAATTCATTTCTCAAGACAGACA 478
QY 480 TAAATGACTGGGAGCGAGCTTGTACTATGCACTTCTTGGCAAGGCAAGCGAGA 539
Db 479 TAAATGACTGGGAGCGAGCTTGTACTATGCACTTCTTGGCAAGGCAAGCGAGA 538
QY 540 ACGTTTACAGACCATGAGGATGCTTCTGATTTGAGTTTGTAGCTCTTGAGCTGCTTA 599
Db 539 ACGTTTACAGACCATGAGGATGCTTCTGATTTGAGTTTGTAGCTCTTGAGCTGCTTA 598
QY 600 CGTGTATGCCATCCACAGAAATCCCAACAAGTGCATTTGTTGAAGAGACCTTGCACT 659
Db 599 CGTGTATGCCATCCACAGAAATCCCAACAAGTGCATTTGTTGAAGAGACCTTGCACT 658
QY 660 GCTTCTACTGCAACTCTGCTGATAGCCCAATGAGGTAATTTCTTATGATTCCTAC 719
Db 659 GCTTCTACTGCAACTCTGCTGATAGCCCAATGAGGTAATTTCTTATGATTCCTAC 718
QY 720 AGTCTGTAAGTGCATAGGTAATCATTTGTGATGTTCCCTTACTATATAGAGATCTG 779
Db 720 AGTCTGTAAGTGCATAGGTAATCATTTGTGATGTTCCCTTACTATATAGAGATCTG 779

Db 719 AGTCTGTAAGTGCATAGGTAATCATTTGTGATGTTCCCTTACTATATAGAGATCTG 778
QY 780 TTATTAATTAATAGATCTGAGACACATTAATAGGTTGATTAATACATCAGACGAA 839
Db 779 TTATTAATTAATAGATCTGAGACACATTAATAGGTTGATTAATACATCAGACGAA 838
QY 840 CATCTGTTAAAGTTATGAATGCTGCTGCTGTAATAAATGATTTTCCCTTCCCTC 899
Db 839 CATCTGTTAAAGTTATGAATGCTGCTGCTGTAATAAATGATTTTCCCTTCCCTC 898
QY 900 TCCAGACTCTGAGATTCCTGCTGCTGCTGTAATAAATGATTTATGATTCAGT 959
Db 899 TCCAGACTCTGAGATTCCTGCTGCTGCTGTAATAAATGATTTATGATTCAGT 958
QY 960 AAAATGATGCGATGAATAAGTAATTTCCCTGTTTAAAGCTGTAATATGATTCATTT 1019
Db 959 AAAATGATGCGATGAATAAGTAATTTCCCTGTTTAAAGCTGTAATATGATTCATTT 1018
QY 1020 GGAATCTATTAATTTCTATATTTGTTTCAATGAGGCTGTAATGCTGTAATTTA 1079
Db 1019 GGAATCTATTAATTTCTATATTTGTTTCAATGAGGCTGTAATGCTGTAATTTA 1078
QY 1080 TAAATATGAGGAATGCTTTTATCAAGTAGAATCCTTTAAACAAGTGAATGAGCTCTT 1139
Db 1079 TAAATATGAGGAATGCTTTTATCAAGTAGAATCCTTTAAACAAGTGAATGAGCTCTT 1138
QY 1140 TCGTATGTTGTTAGTTTGCCTTCCCAAGACATGCTGCA-GGATCTTCCAGAAAG 1198
Db 1139 TCGTATGTTGTTAGTTTGCCTTCCCAAGACATGCTGCA-GGATCTTCCAGAAAG 1197
QY 1199 ATTCCACACTGAGTGAAGAGTGGCTGCTAGTCTCCGTGACGTTCTGCTACTC 1258
Db 1198 ATTCCACACTGAGTGAAGAGTGGCTGCTAGTCTCCGTGACGTTCTGCTACTC 1257
QY 1259 TAAAGTGTTCGAAAGTATTAAGCACTCAGAAATTATTTTGAACCAATGATCAGTAG 1318
Db 1258 TAAAGTGTTCGAAAGTATTAAGCACTCAGAAATTATTTTGAACCAATGATCAGTAG 1317
QY 1319 ACATTAATATATTAACAATGCCCTATATTAATA-TTCTGCATACTTAATAATTATG 1377
Db 1318 ACATTAATATATTAACAATGCCCTATATTAATA-TTCTGCATACTTAATAATTATG 1377
QY 1378 ACTATATGATGGTG-TGATGCAAT-GAATATGCTGCTGATATTAATAATTATAT 1434
Db 1378 ACTATATGATGGTG-TGATGCAAT-GAATATGCTGCTGATATTAATAATTATAT 1433
QY 1435 ATAG-TTATATGCTTAATAGATTAATAAAGTACCAAGCTAGAACCTGTAACAATGAT 1493
Db 1438 ATAGTTTATATGCTTAATAGATTAATAAAGTACCAAGCTAGAACCTGTAACAATGAT 1492
QY 1494 ATGAGTTAATGTAATAGCATTTACACTTCCAAACATTTTTCAGTTACATAATTAA 1553
Db 1498 ATGAGTTAATGTAATAGCATTTACACTTCCAAACATTTTTCAGTTACATAATTAA 1552
QY 1554 GTTATATCCTTTAATAAAGTCCCTCAGTAATCATTAAGCTTCATCTACTTTTGAATAAT 1613
Db 1558 GTTATATCCTTTAATAAAGTCCCTCAGTAATCATTAAGCTTCATCTACTTTTGAATAAT 1612
QY 1614 TTATCTTAATATGTTGTTGTTGCTGCTGTAATAAACAACAATAAAGTCTTTGAGAAGG 1673
Db 1618 TTATCTTAATATGTTGTTGTTGCTGCTGTAATAAACAACAATAAAGTCTTTGAGAAGG 1672
QY 1674 GAACATCATTAATAACCAACAACAAGGCTTAATTTGTTGAGACCAAAATGTTTAATAA 1733
Db 1678 GAACATCATTAATAACCAACAACAAGGCTTAATTTGTTGAGACCAAAATGTTTAATAA 1732
QY 1734 TTATTTTAAATGATTAATAAAGTAAATTAATTTATTTGTTGTAATATGATGTTT 1793
Db 1738 TTATTTTAAATGATTAATAAAGTAAATTAATTTATTTGTTGTAATATGATGTTT 1792
QY 1794 GAAGTATGATATGATGCAAGATGCAATGCAATGCAATTTTATACCTGCTGATTA 1853
Db 1798 GAAGTATGATATGATGCAAGATGCAATGCAATGCAATTTTATACCTGCTGATTA 1852

QY	1854	TTTGCATTTTAAAAATTTTCCATTTTAGCACCAACTGTGCACCTGAAGAAATCTTCAGG	1913
Db	1858	TTTGCAATTTTAAAAATTTTCCATTTTAGCACCAACTGTGCACCTGAAGAAATCTTCAGG	1917
QY	1914	GAATAGGCACACTGGAGAGTCAAACTGTGCAAGGGGGTACTGTGAAAGACTATTCAAAA	1973
Db	1918	GAATAGGCACACTGGAGAGTCAAACTGTGCAAGGGGGTACTGTGAAAGACTATTCAAAA	1977
QY	1974	ACTTGTCCCTTAATAAGAAATACATTGACGGCCAAAAAGTAAGTTACACACATTCATGG	2033
Db	1978	ACTTGTCCCTTAATAAGAAATACATTGACGGCCAAAAAGTAAGTTACACACATTCATGG	2037
QY	2034	AAGCTATATTGTCCCTGGCGTGTCCCTATTCTATGCAATTGACAGTTTCCGTGAATACCT	2093
Db	2038	AAGCTATATTGT - CTGGCTGTCCCTATTCTATGCAATTGACAGTTTCCGTGAATACCT	2096
QY	2094	ATTGTCAATTTTCTTTTTCACAGAAAAAGTGTGAGAGAAAGACGGAGAGTAACCAA	2153
Db	2097	ATTGTCAATTTTCTTTTTCACAGAAAAAGTGTGAGAGAAAGACGGAGAGTAACCAA	2156
QY	2154	TTCCCTAGACTACCTGCAAGAGTTCTTGTTGTAATGAACACCAGAGTGATAATAGAAAGT	2213
Db	2157	TTCCCTAGACTACCTGCAAGAGTTCTTGTTGTAATGAACACCAGAGTGATAATAGAAAGT	2216
QY	2214	TGAGACTAAACTGGTTTGTTCGACGCCAAGAGATTTTGGAGAGAGAAGACATTTTACTCCAG	2273
Db	2217	TGAGACTAAACTGGTTTGTTCGACGCCAAGAGATTTTGGAGAGAGAAGACATTTTACTCCAG	2276
QY	2274	TGAGAAATGAGGGCCCAAGAAAGAGTCAGGCCCTTAATTTTCAATATTAATTAACTTCAGAGG	2333
Db	2277	TGAGAAATGAGGGCCCAAGAAAGAGTCAGGCCCTTAATTTTCAATATTAATTAACTTCAGAGG	2336
QY	2334	GAAAGTAAATATTTTCAGGCACTACTGACACTTTTGCCAGAAAGCATAAATCTTAAATAAT	2393
Db	2337	GAAAGTAAATATTTTCAGGCACTACTGACACTTTTGCCAGAAAGCATAAATCTTAAATAAT	2396
QY	2394	ATTTCAGATATCAGAAATCAATGAAGTATTTTCCCTCCAGGCAAAATTGATATACTTTTTC	2453
Pb	2397	ATTTCAGATATCAGAAATCAATGAAGTATTTTCCCTCCAGGCAAAATTGATATACTTTTTC	2456
QY	2454	TTATTTAACTTAACATTCCTGTAATAATGTCTGTTAACCTTAATAGTATTTATGAATGTTA	2513
Db	2457	TTATTTAACTTAACATTCCTGTAATAATGTCTGTTAACCTTAATAGTATTTATGAATGTTA	2516
QY	2514	ACAATTTGGTAAATTAGTATTTATTTAATGTTATGTGTCTAATAAAAACAAAAATAG	2573
Db	2517	ACAATTTGGTAAATTAGTATTTATTTAATGTTATGTGTCTAATAAAAACAAAAATAG	2576
QY	2574	ACAACCTGTTCAATTTGCTGCTGGCCCTGTCCTTAGCAATTTGAAGTTAGCACAGTCCAT	2633
Db	2577	ACAACCTGTTCAATTTGCTGCTGGCCCTGTC - TTAGCAATTTGAAGTTAGCACAGTCCAT	2634
QY	2634	TGAGTACATGCCCAGTTTGGAGGAAGGCTGTGAGCAACATGTGGCTGAGCATCCCAATTTC	2693
Db	2635	TGAGTACATGCCCAGTTTGGAGGAAGGCTGTGAGCAACATGTGGCTGAGCATCCCAATTTC	2694
QY	2694	TCTGGAGAAGTCTCAAGGTTGCCAAGGCACACACCAGAGGTGGAAGTGATCTAGCAGACTTA	2753
Db	2695	TCTGGAGAAGTCTCAAGGTTGCCAAGGCACACACCAGAGGTGGAAGTGATCTAGCAGACTTA	2754
QY	2754	GTTGGGGATGTGGGGAGCAGGAGACACAGGCAGGAGGTGAACCTGTTTCTCTCAACAGTA	2813
Db	2755	GTTGGGGATGTGGGGAGCAGGAGACACAGGCAGGAGGTGAACCTGTTTCTCTCAACAGTA	2814
QY	2814	TATCCAGAACCTGGGATGCTGAAGGGTAAATGTTAGGGAATTAATGAATGAATGTCTGTT	2873
Db	2815	TATCCAGAACCTGGGATGCT - GCAGGGTAAATGTTAGGGAATTAATGAATGAATGTCTGTT	2873
QY	2874	TCCAAGA - TGATTTAGAACTAAATAGATTGTAAAG - -CTCCCTGGAAGAAGGATGT -	2929
Db	2874	TCCAAGA - TGATTTAGAACTAAATAGATTGTGTAAAGGCGTCCCTCGAAGAAGGCGAGTG	2933

OY	2930	--GGAACCTGTACTAGGTTTCCTTGCCCAGCCTGTGAGAAGAAATTTGGCAGATC-ATCTCA	2986
Db	2934	TGGGAACCTGTAACTAGGTTTCCTGCCAGCCTGTGAGAAGAAATTTGGCAGATCAATCTCA	2993
OY	2987	TTGCCAGTATAGAGAGAGGAAGCCAGAAAACCCTCTCTGCCAAGGCCTGACAGGGTTCTTA--	3044
Db	2994	TTGCCAGTATAGAGAGAGGAAGCCAGAAAACCCTCTCTGCCAAGGCCTGACAGGGTTCTTAAC	3053
OY	3045	CCACCTGACCCCTGCACCATTAACAAAAAGG-ACAGAGAGACA-TGTTAGGGCAGTCCCATT	3102
Db	3054	CCACCTGACCCCTGCACCATTAACAAAAAGGAACAGAGACACTGTTAGGGCAGTCCCATT	3113
OY	3103	GAAAGACTGAGTTCCGTAATTCCC-GGGGACGGGACGACACCGCCGACACAACA-TCCATT	3160
Db	3114	GAAAGACTGAGTTCCGTAATCCCCGGGGGACGGGACGACACCGCCGACACAACACTCCATT	3173
OY	3161	CTGCCCTGCTTATGGCTATCAGTAGCATCAGTCTCTCTGTTTGAGAAACTTCTC	3220
Db	3174	CTGCCCTGCTTATGGCTATCAGTAGCATCAGTCTCTCTGTTTGAGAAAACTTCTC	3233

RESULT 9	
AA071243	
ID	AA071243 standard; DNA; 1395 BP.
XX	
AC	AA071243;
XX	
DT	13-MAY-1991 (first entry)
XX	
DE	Sequence encoding human eosinophil differentiation factor (EDF).
XX	
KW	EDA; B-cell growth factor II; BCGF II; haemopoiesis; myeloma cells;
KW	eosinophilia; interleukin; ds.
XX	
OS	Homo sapiens.
XX	
FH	Key
FT	Location/Qualifiers
FT	42..170
FT	/*tag= a
FT	171..276
FT	/*tag= b
FT	277..371
FT	/*tag= c
XX	
PN	W08704466-A.
XX	
PD	30-JUL-1987.
XX	
PF	15-JAN-1987; 87WO-GB00021.
XX	
PR	15-JAN-1986; 86GB-0000836.
PR	15-JAN-1986; 86GB-0000835.
XX	
PA	(AMER-) AMERSHAM INT PLC.
XX	
PI	Sanderson CJ, Young IG;
XX	
DR	WPI; 1987-221267/31.
DR	P-PSDB; AAP71065.
XX	
PT	Eosinophil differentiation factor - with eosinophil
PT	differentiation activity and B cell growth promoting activity of
PT	B cell growth factor II.
XX	
PS	Disclosure; Fig 4; 37pp; English.
XX	
CC	The EDF gene product is a novel interleukin, useful in the study of
CC	haemopoiesis and B-cell differentiation, and may have utility in MAB
CC	production. It may be used therapeutically in regulation of the immune
CC	response, and promotion of eosinophilia.
XX	
SQ	Sequence 1395 BP; 430 A; 261 C; 313 G; 391 T; 0 other;

Query Match	36.3%	Score 1171.2;	DB 8;	Length 1395;
Best Local Similarity	96.7%	Pred. No. 5.7e-216;		
Matches 1346; Conservative	0;	Mismatches 28;	Indels 18;	Gaps 14;

OY	1842	TTCCTGATTAATTGCATTTTAAAAATTTTCCCTCATTTAGCACCAACTGTGCACGAAG	1901
Db	1	TTTTCTTGATTAATTGCATTTTAAAAATTTTCCCTCATTTAGCACCAACTGTGCACGAAG	60
OY	1902	AAATCTTTCAGGGAAATAGGCACACACTGGAGAGTCAAAGTGTCAAGGGGTACTGTGAAA	1961
Db	61	AAATCTTTCAGGGAAATAGGCACACACTGGAGAGTCAAAGTGTCAAGGGGTACTGTGAAA	120
OY	1962	GACTATTCAAAAACTGTGCTTAAATAAAGAAATACATTGACGGCCAAAAAGTAAGTTACA	2021
Db	121	GACTATTCAAAAACTGTGCTTAAATAAAGAAATACATTGACGGCCAAAAAGTAAGTTACA	180
OY	2022	CACATTCAATGGAAGCTATATTTGTCCCTGCCGTGCTTATTTCTATGGAATTGCAGTTT	2081
Db	181	CACATTCAATGGAAGCTATATTTGT - CTGGCTGTGCTTATTTCTATGGAATTGCAGTTT	239
OY	2082	CCTGTAATACCCTATTGTCAATTTTCTTTTTCACAGAAAAAGTGTGAGAAGAACCGG	2141
Db	240	CCTGTAATACCCTATTGTCAATTTTCTTTTTCACAGAAAAAGTGTGAGAAGAACCGG	299
OY	2142	AGAGTAAACCAATTCCTAGACTACCTGCAAGAGTTTCTGTGTAATGAACCGAGTGG	2201
Db	300	AGAGTAAACCAATTCCTAGACTACCTGCAAGAGTTTCTGTGTAATGAACCGAGTGG	359
OY	2202	ATAATAGAAAGTTGAGACTAAACTGTTTGTGTCAGCCAAAGATTTTGAGAGAGAGAC	2261
Db	360	ATAATAGAAAGTTGAGACTAAACTGTTGTCAGCCAAAGATTTTGAGAGAGAGAGAC	419
OY	2262	ATTTTACTGCAGTGAGATGAGGGCCACAGAAAGAGTCAGGCCCTTAATTTTCAATATAAT	2321
Db	420	ATTTTACTGCAGTGAGATGAGGGCCACAGAAAGAGTCAGGCCCTTAATTTTCAATATAAT	479
OY	2322	TAACTTCAGAGGGAAAGTAATAATTTTCAGGCATCTGCACACTTTGCCAGAAAGCATAAAA	2381
Db	480	TAACTTCAGAGGGAAAGTAATAATTTTCAGGCATCTGCACACTTTGCCAGAAAGCATAAAA	539
OY	2382	TTCCTAAAAATATATTTTCAGATATCAGAAATCATGTAATTTTCTCCAGGCCAAATTGA	2441
Db	540	TTCCTT - AAATATATTTTCAGATATCAGAAATCATGTAATTTTCTCCAGGCCAAATTGA	598
OY	2442	TATACCTTTTCTTATTTTAACTTAACATTCCTGTAAAGTCTGTAACTTAATAGTATTT	2501
Db	599	TATACCTTTTCTTATTTTAACTTAACATTCCTGTAAAGTCTGTAACTTAATAGTATTT	658
OY	2502	ATGAATGTTAAGAAATTTGGTAAATTAGTATTTAATGTTATGTTGTGTTCTAATA	2561
Db	659	ATGAATGTTAAGAAATTTGGTAAATTAGTATTTAATGTTATGTTGTGTTCTAATA	718
OY	2562	AAACAAAAATAGACAACCTGTCAATTTGCTGCTGCCCTCTCCTTAGCAATTTGAAGTT	2621
Db	719	AAACAAAAATAGACAACCTGTCAATTTGCTGCTGCCCTCTCCTTAGCAATTTGAAGTT	777
OY	2622	AGCACAGTCCATTGAGTACATGCCCAGTTTGGAGAGAAAGGCTGAGCACATGTGCTGAG	2681
Db	778	AGCACAGTCCATTGAGTACATGCCCAGTTTGGAGAGAAAGGCTGAGCACATGTGCTGAG	837
OY	2682	CATCCCCCATTTCTCTGGAGAAAGTCTCAAGGTTGCAAGGCACACACAGAGGTGAAGTATC	2741
Db	838	CATCCCCCATTTCTCTGGAGAAAGTCTCAAGGTTGCAAGGCACACACAGAGGT - GAAGTATC	896
OY	2742	TAGCAGGACTTAGTGGGGAGTGTGGGGAGCAGGGACACAGGCAGAGGTGAACCTGCTTTT	2801
Db	897	TAGCAGGACTTAGTGGGGAGTGTGGGGAGCAGGGACACAGGCAGAGGTGAACCTGCTTTT	956
OY	2802	CTCTCTACAGTATATCCAGAACCTGGGATGGTCCGAAGGTTAAATGGTAGGGAATAATGA	2861
Db	957	CTCTCTACAGTATATCCAGAACCTGGGATGGT - GCAGGGTTAAATGGTAGGGAATAATGA	1015
OY	2862	ATGAATGTGTTCCAAGA - TGAATGTAGAACTAAAAATGAGTTGTAAG - CTCCTCTGGA	2918

Db	1016	ATGATGTGCTTCCACAGACTGATGTAGAACTAAATAGTGTGAAGCGTCCCCCTGGA	1075
QY	2919	ACAGGGATGT--GGAACCTGTACTAGGTTCCCTGCCACCCCTGTGAGAAGATTGGC	2975
Db	1076	AGAAAGGACAGTGTGGGAACCTGTAAGTTCCCTCCCAACCCCTGTCAAGAAGATTGGC	1135
QY	2976	AGATC-ATTCATTTGCCAGTATAGAGAGGAAGCCAGAAACCCCTCTCTGCCAAGCCCTGCA	3034
Db	1136	AGATCAATCTCATTTGCCAGTATAGAGAGGAAGCCAGAAACCCCTCTCTGCCAAGCCCTGCA	1195
QY	3035	GGGGTTCTTA--CCACCTGACCCCTGCACCATACCAAAAGG-ACAGAGAGACA-TGGTAGG	3090
Db	1196	GGGGTTCTTACCCCAACCTGACCCCTGCACCATACCAAAAGGAACAGAGACACTGGTAGG	1255
QY	3091	GCAGTCCCATTAGAAGAGACTGAGTTCGGTATTCCC-GGGGCAAGGCAGACACAGGCCGCA	3149
Db	1256	GCAGTCCCATTAGAAGAGACTGAGTTCGGTATTCCCCGGGGGCGAGCGCACACAGGCCGCA	1315
QY	3150	CAACA-TCCATTTCTGCGCTGCTTATGGCTATCAGTAGCATCCTAGAGATTCTTCTGTTTG	3208
Db	1316	CAACACTCCATTTCTGCGCTGCTTATGGCTATCAGTAGCATCCTAGAGATTCTTCTGTTTG	1375
QY	3209	AGAAAACTTCTC 3220	
Db	1376	AGAAAACTTCTC 1387	

RESULT	10
AAH92594	
ID	AAH92594 standard; DNA; 700 BP.
XX	
AC	AAH92594;
XX	
DT	09-OCT-2001 (first entry)
XX	
DE	Human inflammatory bowel disease related gene fragment IGR1294a.
XX	
KW	Human; inflammatory bowel disease; Crohn's disease; ulcerative colitis
KW	single nucleotide polymorphism; SNP; chromosome 19p13; paternity test;
KW	chromosome 5q31-33; forensic test; gene therapy; ds.
XX	
OS	Homo sapiens.
XX	
PN	WO200142511-A2.
XX	
PD	14-JUN-2001.
XX	
PF	11-DEC-2000; 2000WO-US33632.
XX	
PR	10-DEC-1999; 99US-0170257.
PR	10-APR-2000; 2000US-0196046.
XX	
PA	(WHED) WHITEHEAD INST BIOMEDICAL RES.
PA	(ELLI-) ELLIPSIS BIOTHERAPEUTICS CORP.
XX	
PI	Daly M, Hudson TJ, Lander ES, Rioux J, Siminovitch K;
XX	
DR	WPI; 2001-367874/38.
XX	
PT	Testing for the presence of polymorphisms associated with inflammatory
PT	bowel disease, using a hybridization assay -
XX	
PS	Disclosure; Page 262; 463pp; English.
XX	
CC	The present invention describes a method for detecting the presence of
CC	polymorphisms associated with inflammatory bowel diseases such as
CC	ulcerative colitis and Crohn's disease. The methods can be used to dete
CC	the presence of genetic polymorphisms associated with inflammatory bowe
CC	disease and correlating their occurrence with disease states. They may
CC	used in this way for phenotypic correlations, forensics, paternity
CC	testing, medicine and genetic analysis. The present sequence is a gene
CC	containing a polymorphic site described in the exemplification of the

XX Testing for the presence of polymorphisms associated with inflammatory
PT bowel disease, using a hybridization assay -
XX
XX
PS Disclosure; Page 261-262; 463pp; English.
XX
CC The present invention describes a method for detecting the presence of
CC polymorphisms associated with inflammatory bowel diseases such as
CC ulcerative colitis and Crohn's disease. The methods can be used to detect
CC the presence of genetic polymorphisms associated with inflammatory bowel
CC disease and correlating their occurrence with disease states. They may be
CC used in this way for phenotypic correlations, forensics, paternity
CC testing, medicine and genetic analysis. The present sequence is a gene
CC containing a polymorphic site described in the exemplification of the
CC invention.

XX Sequence 700 BP; 216 A; 101 C; 125 G; 258 T; 0 other;

Query Match 19.4%; Score 627.4; DB 22; Length 700;
Best Local Similarity 98.3%; Pred. No. 1.9e-111;
Matches 687; Conservative 0; Mismatches 6; Indels 6; Gaps 5;

OY 748 GTGATGGTCTTCTTACTATATAGAGATCTGTTAAATATAGATTCGACACATT 807
|||||
Db 1 GTGATGGTCTTCTTACTATATAGAGATCTGTTAAATATAGATTCGACACATT 60
OY 808 AGTACATGGGTGATACATACATCACCAGCAACATCTCTGTTAAAGTTATGATGCTGCT 867
|||||
Db 61 AGTACATGGGTGATACATACATCACCAGCAACATCTCTGTTAAAGTTATGATGCTGCT 120
OY 868 GTGCTGTAAAAATGATGTATTTCTCTCTCCAGACTCTGAGGATTCCTCTCTCT 927
|||||
Db 121 GTGCTGTAAAAATGATGTATTTCTCTCTCCAGACTCTGAGGATTCCTCTCTCT 180
OY 928 ACATAAAAATGATGTTAAATATGATTCAGTAAATGATGGCATGATGATGATTTTC 987
|||||
Db 181 ACATAAAAATGATGTTAAATATGATTCAGTAAATGATGGCATGATGATGATTTTC 240
OY 988 CTGTTTAAAGCTGTTAAATCATTTAGTTATCATTTGGAATTTTATTTTGT 1047
|||||
Db 241 CTGTTTAAAGCTGTTAAATCATTTAGTTATCATTTGGAATTTTATTTTGT 300
OY 1048 TTCATATGGGTGGTGTGATGCTGTACTTATAAATATGAGGATGCTTTTATCAAG 1107
|||||
Db 301 TTCATATGGGTGGTGTGATGCTGTACTTATAAATATGAGGATGCTTTTATCAAG 360
OY 1108 TAGAATCCTTTAAACAGTGGATTAGGCTCTTGGTGATGTTGTTAGTTTCCCTCCAA 1167
|||||
Db 361 TAGAATCCTTTAAACAGTGGATTAGGCTCTTGGTGATGTTGTTAGTTTCCCTCCAA 419
OY 1168 AGAGCATCGTGTCA-GGATTTCTTCCAGAGGATTCACACTGAGTGAGAGTGGCTGCT 1226
|||||
Db 420 AGAGCATCGTGTCAAGGATTTCTTCCAGAGGATTCACACTGAGTGAGAGTGGCTGCT 479
OY 1227 AGTCTCCGTGAGTGTGACTCTTCTCAGCTTAAAGTGTCTTCTGAAGTATAGCAACT 1286
|||||
Db 480 AGTCTCCGTGAGTGTGACTCTTCTCAGCTTAAAGTGTCTTCTGAAGTATAGCAACT 539
OY 1287 CAGAATTTATTTTGAACCATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1346
|||||
Db 540 CAGAATTTATTTTGAACCATGATGATGATGATGATGATGATGATGATGATGATGATGAT 599
OY 1347 ATTAATAA-TTCTGCACTTAAATATATGATGATGATGATGATGATGATGATGATGATGAT 1402
|||||
Db 600 ATTAATAA-TTCTGCACTTAAATATATGATGATGATGATGATGATGATGATGATGATGAT 659
OY 1403 AATATGCTGTGATATTAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1441
|||||
Db 660 AATATGCTGTGATATTAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 698

RESULT 14
ABL33045/c

ID ABL33045 standard; DNA; 5397 BP.
XX
AC ABL33045;
XX
DT 26-MAR-2002 (first entry)
XX
DE Human immune system associated gene SEQ ID NO: 1018.
XX

KW Human; immune system disease; cytosine methylation; antiasthmatic;
KW antiarteriosclerotic; anti-anaemic; cytosolic; nootropic;
KW neuroprotective; anti-HIV; anticonvulsant; ophthalmological;
KW antirheumatic; antiarthritic; antidiabetic; antipsoriatic;
KW antineoplastic; cancer; eye disease; arteriosclerosis; anaemia;
KW acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;
KW neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;
KW gene; ds.

OS Homo sapiens.
XX
PN WO200200928-A2.
XX
PD 03-JAN-2002.
XX
PF 02-JUL-2001; 2001WO-EP07537.
XX
PR 30-JUN-2000; 2000DE-1032529.
PR 01-SEP-2000; 2000DE-1043826.
XX
PA (EPIC-) EPIGENOMICS AG.

PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2002-130909/17.
XX

PT Nucleic acid comprising fragment of chemically modified gene, useful
PT for diagnosis and treatment of diseases associated with abnormal
PT cytosine methylation -
XX

PS Claim 1; SEQ ID NO 1018; 32pp + Sequence Listing; German.

CC The present invention provides a number of human immune system associated
CC genes which are modified by the methylation of cytosines. The sequences
CC can be used in the diagnosis and treatment of immune system disorders,
CC including eye diseases such as retinopathy, neovascular glaucoma and
CC macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid
CC leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis,
CC rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel
CC diseases. The present sequence is a gene of the invention.
XX

XX Sequence 5397 BP; 1638 A; 50 C; 1159 G; 2550 T; 0 other;

Query Match 19.4%; Score 626; DB 24; Length 5397;
Best Local Similarity 82.9%; Pred. No. 5.2e-111;
Matches 751; Conservative 0; Mismatches 150; Indels 5; Gaps 3;

OY 1 ATCTAATCAAGACCCAGTGAACAGACTGACCTGGCAAGGCTTGGC-ATTTCATT 59
|||||
Db 902 ATCTAATCAAGACCCAGTGAACAGACTGACCTGGCAAGGCTTGGC-ATTTCATT 843
OY 60 TCAATCAGTCTCTCCACAGATTTTCAATTTCTTTAAGACAGATTATCTAGCCAC 119
|||||
Db 842 TCAATCAGTCTCTCCACAGATTTTCAATTTCTTTAAGACAGATTATCTAGCCAC 783
OY 120 AGTCATAGTAGACATAGCCGATCTGAAAAAACAATCCCAATATTATGATTTAG 179
|||||
Db 782 AATCATATTAATAACATTAACCGATCT-AAAAAACAATCCCAATATTATATTAA 725
OY 180 CATAAATCTGTTAGTGTGCTACCTTACTTTGTTGACACATCTTTAAGAGGA 239
|||||
Db 724 CATAAATCTGTTAGTGTGCTACCTTACTTTGTTGACACATCTTTAAGAGGA 665
OY 240 AGTTAATTTCTGATTTTAAAGAAATGCAATGTGGGCAATGATGATTAACCAAGAT 299
|||||

Db 664 AATTAAATTTCTAATTTTAAAAATACAAATATAAACAAATATATATTAAACCAAAAAAT 605
 QY 300 TCCCTCCGTAATAGAAAATGTTTAAAGGGGAGGAGGATTTTATTATTAAGA 359
 Db 604 TCC-TTCGTAATTAATAATATTTTAAAAAATTTTAAAAAATTTTATTAATAA 547
 QY 360 TAAAGTAATTTATTTTAAAGATTAAGGATTTGAACATTTAGTTTACAGATATGC 419
 Db 546 TAAAAATTAATTTATTTTAAATTAATAACATTTAAAAACATTTTATTCAGATATAC 487
 QY 420 CATATTAAGGATTTCTCTATCTGATTTGTAGAAATTTATTCATTTCTCAAGACAGACA 479
 Db 486 CATATTAACATTTCTCTATCTAATTTATTAATAATTTATTCATTTCTCAAAACAAACA 427
 QY 480 TAAATGACTGGGAGGAGGAGTCTTACTATGACATTTCTTGGCCAAAGGCAACGAGA 539
 Db 426 TAAATTAATAAAGGAGGAGGAGTCTTACTATGACATTTCTTGGCCAAAGGCAACGAGA 367
 QY 540 AGCTTCAGAGGAGGAGGAGTCTTCTGATTTGATTTGATTTGATTTGATTTGATTTG 599
 Db 366 AGCTTCAGAGGAGGAGGAGTCTTCTGATTTGATTTGATTTGATTTGATTTGATTTG 307
 QY 600 CGTGTATGAGGAGGAGGAGGAGTCTTCTGATTTGATTTGATTTGATTTGATTTGATTTG 659
 Db 306 CGTGTATGAGGAGGAGGAGGAGTCTTCTGATTTGATTTGATTTGATTTGATTTGATTTG 247
 QY 660 GCTTCTACTCATCGAAGTCTGCTGATTAAGGAGGAGTCTTCTGATTTGATTTGATTTGATTTG 719
 Db 246 ACTTCTACTCATCGAAGTCTGCTGATTAAGGAGGAGTCTTCTGATTTGATTTGATTTGATTTG 187
 QY 720 AGTCTGTAAGTGCATAGGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTG 779
 Db 186 AATCTAATAAATACATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 127
 QY 780 TTATTAATAAATAGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTG 839
 Db 126 TTATTAATAAATAGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTG 67
 QY 840 CATCTGTTAAAGTATGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTG 899
 Db 66 CATCTAATAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 7
 QY 900 TCCAGA 905
 Db 6 TCCAAA 1

RESULT 15
 AAH92595
 ID AAH92595 standard; DNA; 700 BP.
 XX

AC AAH92595;
 XX
 DT 09-OCT-2001 (first entry)
 XX
 DE Human inflammatory bowel disease related gene fragment IGR1295a.
 XX
 KW Human; inflammatory bowel disease; Crohn's disease; ulcerative colitis;
 KW single nucleotide polymorphism; SNP; chromosome 19p13; paternity test;
 KW chromosome 5q31-33; forensic test; gene therapy; ds.
 XX
 OS Homo sapiens.
 XX
 PN WO200142511-A2.
 XX
 PD 14-JUN-2001.
 XX
 PF 11-DEC-2000; 2000WO-US33632.
 XX
 PR 10-DEC-1999; 99US-0170257.
 PR 10-APR-2000; 2000US-0196046.
 XX
 PA (WHED.) WHITEHEAD INST BIOMEDICAL RES.

PA (ELLI-) ELLIPSIS BIOTHERAPEUTICS CORP.
 XX
 PI Daly M, Hudson TJ, Lander ES, Rioux J, Siminovitch K;
 XX
 DR WPI; 2001-367874/38.
 XX
 PT Testing for the presence of polymorphisms associated with inflammatory
 PT bowel disease, using a hybridization assay -
 XX
 PS Disclosure; Page 262-263; 463pp; English.
 XX
 CC The present invention describes a method for detecting the presence of
 CC polymorphisms associated with inflammatory bowel diseases such as
 CC ulcerative colitis and Crohn's disease. The methods can be used to detect
 CC the presence of genetic polymorphisms associated with inflammatory bowel
 CC disease and correlating their occurrence with disease states. They may be
 CC used in this way for phenotypic correlations, forensics, paternity
 CC testing, medicine and genetic analysis. The present sequence is a gene
 CC containing a polymorphic site described in the exemplification of the
 CC invention.
 XX
 SO Sequence 700 BP; 220 A; 104 C; 168 G; 207 T; 1 other;
 Query Match 19.3%; Score 622.4; DB 22; Length 700;
 Best Local Similarity 97.4%; Pred. No. 1.8e-110;
 Matches 675; Conservative 0; Mismatches 12; Indels 6; Gaps 4;
 QY 2241 AAGATTTTGAGAGAGAGACATTTTACTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2300
 Db 1 AAGATTTTGAGAGAGAGAGACATTTTACTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 60
 QY 2301 GCCTTAATTTTCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 2360
 Db 61 GCCTTAATTTTCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 120
 QY 2361 ACTTGCCAG 2420
 Db 121 ACTTGCCAG 180
 QY 2421 TTTTCTCCAG 2480
 Db 181 TTTTCTCCAG 240
 QY 2481 TCTGTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 2540
 Db 241 TCTGTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 300
 QY 2541 ATGTTATGTTGTTCTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 2600
 Db 301 ATGTTATGTTGTTCTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 360
 QY 2601 TGTCTTAAGCAATTTGAAGTTAGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2660
 Db 361 TGTCTTAAGCAATTTGAAGTTAGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 418
 QY 2661 GTCTGAGACAG 2720
 Db 419 GTCTGAGACAG 478
 QY 2721 ACACAG 2780
 Db 479 ACACAG 538
 QY 2781 GCAG 2840
 Db 539 GCAG 597
 QY 2841 TAAATGAG 2899
 Db 598 TAAATGAG 657
 QY 2900 AGTGTAG 2930

Thu Apr 24 08:08:15 2003

us-09-800-629a-78.rng

Page 23

Db 658 AGTTGTAGCGCTCCCCCTGGAAGAAGGCGCAGTG 690

Search completed: April 23, 2003, 23:42:34
Job time : 751 secs

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OM nucleic - nucleic search, using sw model

Run on: April 23, 2003, 23:30:07 ; Search time 120 Seconds
(without alignments)
8254.716 Million cell updates/sec

Title: US-09-800-629A-78
Perfect score: 3230
Sequence: 1 atcctaatacaagaccacagtl.....aaactctctcaagatcc 3230

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Query Match	Length	DB ID	Description
	1	3230	100.0	3230	3	US-09-280-799-78
	2	3230	100.0	3230	6	5324640-1
	3	479.4	14.8	816	3	US-09-079-839-2
	4	360	11.1	1328	1	US-08-592-126-94
	5	161.8	5.0	6727	3	US-08-629-643A-5
	6	161.8	5.0	6727	3	US-09-280-799-1
	7	161.8	5.0	6727	4	US-09-155-884-5
	8	126.8	3.9	377	4	US-09-180-864-1
	9	100	3.1	1534	3	US-08-629-643A-4
	10	100	3.1	1534	4	US-09-155-884-4
	11	59.8	1.9	168575	4	US-09-426-290-1
	12	59.2	1.8	837	4	US-08-998-416-288
	13	56.6	1.8	663	1	US-07-624-313-3
	14	56.2	1.7	636	4	US-08-998-416-1137
	15	54.6	1.7	19124	2	US-08-487-826B-13
	16	54	1.7	5852	1	US-07-867-106-2
	17	53	1.6	7218	1	US-08-232-463-14
	18	50.2	1.6	5852	1	US-07-867-106-2
	19	50	1.5	50	1	US-08-171-389-214
	20	50	1.5	50	1	US-08-123-936-214
	21	50	1.5	50	2	US-08-475-228A-214
	22	50	1.5	50	3	US-08-482-080A-214
	23	50	1.5	50	4	US-09-354-947-214
	24	50	1.5	50	5	PCT-US93-12388-214
	25	50	1.5	1864	4	US-09-468-265-4
	26	49.8	1.5	19124	2	US-08-487-826B-13
	27	49.8	1.5	169998	4	US-09-676-610B-24

28	49.4	1.5	615	4	US-08-998-416-186	Sequence 186, App	
C	29	49.4	1.5	665	2	US-08-883-795A-36	Sequence 36, Appl
	30	49.2	1.5	837	4	US-08-998-416-288	Sequence 288, App
C	31	48.8	1.5	701	4	US-08-998-416-701	Sequence 701, App
C	32	48.2	1.5	615	4	US-08-998-416-186	Sequence 186, App
C	33	48.2	1.5	636	4	US-08-998-416-1137	Sequence 1137, App
C	34	48.2	1.5	3350	3	US-09-110-116-2	Sequence 2, Appl
C	35	47.6	1.5	731	1	US-08-451-405A-2	Sequence 2, Appl
C	36	47	1.5	662	4	US-08-998-416-185	Sequence 185, App
C	37	47	1.5	860	4	US-08-998-416-287	Sequence 287, App
C	38	46.8	1.4	711	4	US-08-998-416-786	Sequence 786, App
C	39	46.2	1.4	665	4	US-08-998-416-937	Sequence 937, App
C	40	46.2	1.4	711	4	US-08-998-416-786	Sequence 786, App
C	41	46.2	1.4	724	4	US-08-998-416-683	Sequence 683, App
C	42	46.2	1.4	732	4	US-08-998-416-1036	Sequence 1036, App
C	43	46.2	1.4	828	4	US-08-998-416-538	Sequence 538, App
C	44	46.2	1.4	834	4	US-08-998-416-305	Sequence 305, App
C	45	46.2	1.4	1864	4	US-09-468-265-4	Sequence 4, Appl

ALIGNMENTS

RESULT 1									
US-09-280-799-78									
Sequence 78, Application US/09280799									
Patent No. 6136603									
GENERAL INFORMATION:									
APPLICANT: Dean, Nicholas M.									
APPLICANT: Karras, James G									
APPLICANT: McKay, Robert									
TITLE OF INVENTION: ANTISENSE MODULATION OF INTERLEUKIN-5 SIGNAL									
FILE REFERENCE: ISPH-0340									
CURRENT APPLICATION NUMBER: US/09/280,799									
CURRENT FILING DATE: 1999-03-26									
NUMBER OF SEQ ID NOS: 208									
SOFTWARE: PatentIn Ver. 2.0									
SEQ ID NO 78									
LENGTH: 3230									
TYPE: DNA									
ORGANISM: Homo sapiens									
US-09-280-799-78									
Query Match									
Best Local Similarity 100.0%; Score 3230; DB 3; Length 3230;									
Matches 3230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
QY	1	ATCCTAATCAAGACCCAGTGAACAGAACTGACCTGCCAAGGCTTGCAATTCATT	60						
DB	1	ATCCTAATCAAGACCCAGTGAACAGAACTGACCTGCCAAGGCTTGCAATTCATT	60						
QY	61	CAATCACTGTCTCCACCACTATTTTCAATTTCTTTAAGACAGATTAACTAGCCACA	120						
DB	61	CAATCACTGTCTCCACCACTATTTTCAATTTCTTTAAGACAGATTAACTAGCCACA	120						
QY	121	GTCATAGTAGAAGACATAGCCGATCTTGAAAAAACAATCCCAATATTTATGATTTAGC	180						
DB	121	GTCATAGTAGAAGACATAGCCGATCTTGAAAAAACAATCCCAATATTTATGATTTAGC	180						
QY	181	ATAAATTTCTGTTAGTGTCTACCTTATCTTTGTTTGCACACATCTTTAAGAGAA	240						
DB	181	ATAAATTTCTGTTAGTGTCTACCTTATCTTTGTTTGCACACATCTTTAAGAGAA	240						
QY	241	GTTAATTTCTGATTTTAAAGAAATGCAATGTGGGCAATGATGATTAACCAAGATT	300						
DB	241	GTTAATTTCTGATTTTAAAGAAATGCAATGTGGGCAATGATGATTAACCAAGATT	300						
QY	301	CTTCCGTAATAGAAAAATGTTTAAAGGGGGGGAACAGGATTTTATTAATAAAGAT	360						
DB	301	CTTCCGTAATAGAAAAATGTTTAAAGGGGGGGAACAGGATTTTATTAATAAAGAT	360						
QY	361	AAAGTAATTTATTTTAAAGATATAAGGACATGGAACAATTTAGTTTACAGATATGCC	420						

Db 361 AAAAGTAAATTTATTTTAAAGATTAAGGCAATTTAGTTCCAGCATATGCC 420
QY 421 ATTATAGGCATTTCTATCTGATTTGTTAGAAATTAATTCATTTCTCAAGACAGACAAT 480
Db 421 ATTATAGGCATTTCTATCTGATTTGTTAGAAATTAATTCATTTCTCAAGACAGACAAT 480
QY 481 AAATGACTGGGAGCGAGCTCTGTACTATGACATTTCTTGGCCAAAGGCAAGCAGAA 540
Db 481 AAATGACTGGGAGCGAGCTCTGTACTATGACATTTCTTGGCCAAAGGCAAGCAGAA 540
QY 541 CGTTTCAGAGCCATGAGGATGCTTCTGCAATTTGAGTTTCTAGCTCTTGAGCTGCTTAC 600
Db 541 CGTTTCAGAGCCATGAGGATGCTTCTGCAATTTGAGTTTCTAGCTCTTGAGCTGCTTAC 600
QY 601 GTGTATGCCATCCCAAGAAATCCCAAGAGTGCATTTGTTGAAAGAGACCTTGGCACTG 660
Db 601 GTGTATGCCATCCCAAGAAATCCCAAGAGTGCATTTGTTGAAAGAGACCTTGGCACTG 660
QY 661 CTTTCTACTCATCGAAGCTCTGCTGATAGCCCAATGAGTAATTTCTTATGATTCCTACA 720
Db 661 CTTTCTACTCATCGAAGCTCTGCTGATAGCCCAATGAGTAATTTCTTATGATTCCTACA 720
QY 721 GTCTGTAAAGTGCATAGGTAATTCATTTGTGATGGTTCCTTACTATATAGAGATCTGT 780
Db 721 GTCTGTAAAGTGCATAGGTAATTCATTTGTGATGGTTCCTTACTATATAGAGATCTGT 780
QY 781 TATATAATATAAGATTCGAGACATTTAGTACATGGGTGATTAACATCACCAGCAAAAC 840
Db 781 TATATAATATAAGATTCGAGACATTTAGTACATGGGTGATTAACATCACCAGCAAAAC 840
QY 841 ATCTGTATAAAGTATGAACTGCTGCTGCTGTAATAATGATTTCTTCCCTTCTCT 900
Db 841 ATCTGTATAAAGTATGAACTGCTGCTGCTGTAATAATGATTTCTTCCCTTCTCT 900
QY 901 CCAGACTCTGAGGATTCCTGCTCTGTACATAAAAATGTAAGTTAATTATGATTCAGTA 960
Db 901 CCAGACTCTGAGGATTCCTGCTCTGTACATAAAAATGTAAGTTAATTATGATTCAGTA 960
QY 961 AAATGATGCGATGAATAAGTAATTTCTGTTTAAAGCTGTAATCATTTAGTTATCATTTG 1020
Db 961 AAATGATGCGATGAATAAGTAATTTCTGTTTAAAGCTGTAATCATTTAGTTATCATTTG 1020
QY 1021 GAACATATTTAATTTCTATATTTTGTTCATATGGGTGCTGTGAATGCTGTACTTAT 1080
Db 1021 GAACATATTTAATTTCTATATTTTGTTCATATGGGTGCTGTGAATGCTGTACTTAT 1080
QY 1081 AAATATGAGGAATGACTTTTATCAAGTAGAATCCTTTAAACAAGTGATTAAGCTCTTT 1140
Db 1081 AAATATGAGGAATGACTTTTATCAAGTAGAATCCTTTAAACAAGTGATTAAGCTCTTT 1140
QY 1141 GGTGATGTTGTTAGTTGCTTCCCAAGAGCATGCTGTCAGGATTTCTTCCAGAAAGAT 1200
Db 1141 GGTGATGTTGTTAGTTGCTTCCCAAGAGCATGCTGTCAGGATTTCTTCCAGAAAGAT 1200
QY 1201 TCCACACTGAGTGAGAGGTGCTGCTAGTCTCCGTCAGTCTGACTCTTTCACACTCTA 1260
Db 1201 TCCACACTGAGTGAGAGGTGCTGCTAGTCTCCGTCAGTCTGACTCTTTCACACTCTA 1260
QY 1261 ACGTGTCTCTGAAGATATTTAGCAACTCAGAATTAATTTTGAACCATGATCAGTAGAC 1320
Db 1261 ACGTGTCTCTGAAGATATTTAGCAACTCAGAATTAATTTTGAACCATGATCAGTAGAC 1320
QY 1321 ATTAATAATATATACAAATGCCCTATATTAATTAATTCGCACTACTTAATATATATGACT 1380
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QY 1381 ATATGATGGTGTGATGCAATGATGCTGCTGATTAATAAATGTAATAATATATAGTT 1440
Db 1381 ATATGATGGTGTGATGCAATGATGCTGCTGATTAATAAATGTAATAATATATAGTT 1440
QY 1441 TATTAGTCTAATAGAAATAAACTACAGCTAGAACTGTAGAAACACATGATGATGAGTT 1500
Db 1441 TATTAGTCTAATAGAAATAAACTACAGCTAGAACTGTAGAAACACATGATGATGAGTT 1500

Db 1441 TATTAGTCTAATAGAAATAAACTACAGCTAGAACTGTAGAAACACATGATGAGTT 1500
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Db 1501 TAATGATATAATGCATTTACACTTCCAAACAATTTTTTCCAGTTACATTAATTAAGTTATAT 1560
QY 1561 CCTTTATAAACTCCTCAGTAATCATATAAGCTTCATCTACTTTTTTGAATAATTTATCTT 1620
Db 1561 CCTTTATAAACTCCTCAGTAATCATATAAGCTTCATCTACTTTTTTGAATAATTTATCTT 1620
QY 1621 AATATGTGGTGGTTTGTGCTAGAAAAACAACAAAACTCTTTGGAGAGGGAAGTCA 1680
Db 1621 AATATGTGGTGGTTTGTGCTAGAAAAACAACAAAACTCTTTGGAGAGGGAAGTCA 1680
QY 1681 TGTAAATACCAAAACAAGCCCTAAGTTGTGGAACCAAAATGTTTAATTAATTAATTTT 1740
Db 1681 TGTAAATACCAAAACAAGCCCTAAGTTGTGGAACCAAAATGTTTAATTAATTAATTTT 1740
QY 1741 TTAATGATGAATTAATAAAGTATATATATTTATTTGTATACAAATATGATGTTTGAAGTAT 1800
Db 1741 TTAATGATGAATTAATAAAGTATATATATTTATTTGTATACAAATATGATGTTTGAAGTAT 1800
QY 1801 GTATACATTCGAGAATGGAACAATGGAACCAAAATTTTATACCTTGCTGTATTTTGCAT 1860
Db 1801 GTATACATTCGAGAATGGAACAATGGAACCAAAATTTTATACCTTGCTGTATTTTGCAT 1860
QY 1861 TTTAAAAATTTTCTCATTTTAGCACCAACTGTGCACCTGAAGAAATCTTTCAGGGAATAGG 1920
Db 1861 TTTAAAAATTTTCTCATTTTAGCACCAACTGTGCACCTGAAGAAATCTTTCAGGGAATAGG 1920
QY 1921 CACACTGGAGAGTCAAACTGTGCAAGGGGGTACTGTGGAAGAAGTATTCAAAACTTGTCTC 1980
Db 1921 CACACTGGAGAGTCAAACTGTGCAAGGGGGTACTGTGGAAGAAGTATTCAAAACTTGTCTC 1980
QY 1981 CTTAATAAAGAAATACATTTGACGGGCCAAAAAGTAAGTTACACACATTCATGGAAGCTAT 2040
Db 1981 CTTAATAAAGAAATACATTTGACGGGCCAAAAAGTAAGTTACACACATTCATGGAAGCTAT 2040
QY 2041 ATTTGCTGCTGCTGCTGCTATTTCTATGAAATTTGACAGTTTCTGTAATACCTATTTGCA 2100
Db 2041 ATTTGCTGCTGCTGCTGCTATTTCTATGAAATTTGACAGTTTCTGTAATACCTATTTGCA 2100
QY 2101 TTTTCTTTTTCACAGAAAAAGTGTGAGAAAGAAAGAGCGAGATTAACCAATTCCTAG 2160
Db 2101 TTTTCTTTTTCACAGAAAAAGTGTGAGAAAGAAAGAGCGAGATTAACCAATTCCTAG 2160
QY 2161 ACTACCTGCAAGAGTTTCTTGTGTAATGAACACCCGAGTGATTAAGAAAGTTGAGACT 2220
Db 2161 ACTACCTGCAAGAGTTTCTTGTGTAATGAACACCCGAGTGATTAAGAAAGTTGAGACT 2220
QY 2221 AAACCTGGTTTGTTCAGAGCCAAAGATTTTGGAGGAGAGAGACATTTACTGCAGTGAAGAT 2280
Db 2221 AAACCTGGTTTGTTCAGAGCCAAAGATTTTGGAGGAGAGAGACATTTACTGCAGTGAAGAT 2280
QY 2281 GAGGGCCAGAAAGAGTCAAGGCCCTTAATTTCAATATATAATTTAACTTCAGAGGGAAGTA 2340
Db 2281 GAGGGCCAGAAAGAGTCAAGGCCCTTAATTTCAATATATAATTTAACTTCAGAGGGAAGTA 2340
QY 2341 AATATTTCAAGGCATCTGACACTTTGCCAGAAAGCATAAATCTTAAATAATATTTACAG 2400
Db 2341 AATATTTCAAGGCATCTGACACTTTGCCAGAAAGCATAAATCTTAAATAATATTTACAG 2400
QY 2401 ATATCAGAAATCAATGAAGTATTTTCTCCAGGCAAAATGATATACTTTTCTATTTTA 2460
Db 2401 ATATCAGAAATCAATGAAGTATTTTCTCCAGGCAAAATGATATACTTTTCTATTTTA 2460
QY 2461 ACTTAACATTCCTGTAATAATGCTGTGTTAACTTAATAGTATTTATGAATGTTAAGAAATTT 2520
Db 2461 ACTTAACATTCCTGTAATAATGCTGTGTTAACTTAATAGTATTTATGAATGTTAAGAAATTT 2520
QY 2521 GGTAAATTAAGTATTTATTTAATGTTATGTTGTGTTCTTAATAAACAACAAATAGACAACCTG 2580
Db 2521 GGTAAATTAAGTATTTATTTAATGTTATGTTGTGTTCTTAATAAACAACAAATAGACAACCTG 2580

QY 2581 TTCAATTGCTGCTGGCCTCTGCTCTTAGCAATTGAGTTAGACAGTCCATTTAGTAC 2640
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Db 2581 TTCAATTGCTGCTGGCCTCTGCTCTTAGCAATTGAGTTAGACAGTCCATTTAGTAC 2640
QY 2641 ATGCCAGTTTGGAGGAGGGTCTGACACATGTGGCTGAGCATCCCATTTCTCTGAG 2700
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Db 2641 ATGCCAGTTTGGAGGAGGGTCTGACACATGTGGCTGAGCATCCCATTTCTCTGAG 2700
QY 2701 AAGTCTCAAGTTGCAAGGACACAGAGGTGGAAGTGAATGATCTAGCAGGACTTAGTGGGA 2760
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Db 2701 AAGTCTCAAGTTGCAAGGACACAGAGGTGGAAGTGAATGATCTAGCAGGACTTAGTGGGA 2760
QY 2761 TGTGGGAGCAGGAGACACAGGAGGTGAACCTGTTTCTCTCTACAGTATATCCAG 2820
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Db 2761 TGTGGGAGCAGGAGACACAGGAGGTGAACCTGTTTCTCTCTACAGTATATCCAG 2820
QY 2821 AACCTGGATGTCGAAAGGTAATGTTAGGGAATAAATGAATGAATGTCGTTCCAGA 2880
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Db 2821 AACCTGGATGTCGAAAGGTAATGTTAGGGAATAAATGAATGAATGTCGTTCCAGA 2880
QY 2881 TGATTTGTAACCTAAATGAGTTGTAAGCTCCCTGGAAGAAGGATGTGGAACCTGTA 2940
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Db 2881 TGATTTGTAACCTAAATGAGTTGTAAGCTCCCTGGAAGAAGGATGTGGAACCTGTA 2940
QY 2941 CTAGGTTCTGCCAGCCTGTGAGAGAATTTGGCAGATCATCTCATTTGCCAGTATAG 3000
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Db 2941 CTAGGTTCTGCCAGCCTGTGAGAGAATTTGGCAGATCATCTCATTTGCCAGTATAG 3000
QY 3001 AGGAAGCAGAAACCTCTCTGCAAGGCTGACAGGGGTTCTTACCACTGACCTGAC 3060
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Db 3001 AGGAAGCAGAAACCTCTCTGCAAGGCTGACAGGGGTTCTTACCACTGACCTGAC 3060
QY 3061 CATAACAAAGAGACAGAGACATGTAGGCGAGTCCCATTTAGAAAGACTGAGTCCGTA 3120
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Db 3061 CATAACAAAGAGACAGAGACATGTAGGCGAGTCCCATTTAGAAAGACTGAGTCCGTA 3120
QY 3121 TTCCCGGCGAGGCGACACAGGCGCACACATCCATTCCTGCTTATGGCTATCA 3180
|||||
Db 3121 TTCCCGGCGAGGCGACACAGGCGCACACATCCATTCCTGCTTATGGCTATCA 3180
QY 3181 GTAGCATCATAGATTTCTGTTTGAGAAACTTCTCTCAAGGATCC 3230
|||||
Db 3181 GTAGCATCATAGATTTCTGTTTGAGAAACTTCTCTCAAGGATCC 3230
.
RESULT 2
5324640-1
; Patent No. 5324640
; APPLICANT: Honjo, Tasuku; Takatsu, Kiyoshi; Severinson, Eva
; TITLE OF INVENTION: HUMAN B-CELL DIFFERENTIATION FACTOR AND
; PROCESS OF PRODUCING SAID FACTOR
; NUMBER OF SEQUENCES: 2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/99,467
; FILING DATE: 21-SEP-1987
; SEQ ID NO:1:
; LENGTH: 3230
5324640-1
Query Match 100.0%; Score 3230; DB 6; Length 3230;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 121 GTCATAGTAGAACAATAGCCGATCTTGAAAAAACAATTCACATATATTATTTAGC 180
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QY 181 ATAAATTTCTGTTAGTGTCTACCTTATACCTTTTGCACACATCTTTAAGAGAA 240
|||||
Db 181 ATAAATTTCTGTTAGTGTCTACCTTATACCTTTTGCACACATCTTTAAGAGAA 240
QY 241 GTTAATTTCTGATTTTAAAGAAATGCAATGTGGGCAATGATGATTAACCAAGATT 300
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Db 241 GTTAATTTCTGATTTTAAAGAAATGCAATGTGGGCAATGATGATTAACCAAGATT 300
QY 301 CCTCCGTAATAGAAAATGTTTAAAGGGGGAACAGGATTTTATTAATAAGAT 360
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Db 301 CCTCCGTAATAGAAAATGTTTAAAGGGGGAACAGGATTTTATTAATAAGAT 360
QY 361 AAAAGTAATTTATTTTAAAGATATAGGCAATGGAACATTTAGTTTACGATATGCC 420
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Db 361 AAAAGTAATTTATTTTAAAGATATAGGCAATGGAACATTTAGTTTACGATATGCC 420
QY 421 ATTTATGCAATTTCTATCTGATTTGTAAGAAATTTATTTCTCTCAAGACAGCAAT 480
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Db 421 ATTTATGCAATTTCTATCTGATTTGTAAGAAATTTATTTCTCTCTCAAGACAGCAAT 480
QY 481 AAATGACTGGGAGCAGCTCTGTACTATGCACTTTCTTGGCAAGGCAACGACAGAA 540
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Db 481 AAATGACTGGGAGCAGCTCTGTACTATGCACTTTCTTGGCAAGGCAACGACAGAA 540
QY 541 CGTTTCAGAGCCATGAGATGCTTCTGCAATTTGAGTTTGTAGCTCTGAGCTGCTAC 600
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Db 541 CGTTTCAGAGCCATGAGATGCTTCTGCAATTTGAGTTTGTAGCTCTGAGCTGCTAC 600
QY 601 GTGTATGCCATCCCCACAGAAATTCACACAGTGCATTTGTAAGAGACCTGGCACTG 660
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Db 601 GTGTATGCCATCCCCACAGAAATTCACACAGTGCATTTGTAAGAGACCTGGCACTG 660
QY 661 CTTTCTACTCATCGAATCTGCTGTATAGCCAAATGAGTAATTTCTTTATGATTCCTACA 720
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Db 661 CTTTCTACTCATCGAATCTGCTGTATAGCCAAATGAGTAATTTCTTTATGATTCCTACA 720
QY 721 GTCTGTAAAGTGCATAGTAATCATTTGTGATGCTTCTTACTATATATAGAGATCTGT 780
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Db 721 GTCTGTAAAGTGCATAGTAATCATTTGTGATGCTTCTTACTATATATAGAGATCTGT 780
QY 781 TATTAATATATAGATTTGAGCACATATAGTATGAGTATACATCACGCAAC 840
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Db 781 TATTAATATATAGATTTGAGCACATATAGTATGAGTATACATCACGCAAC 840
QY 841 ATTCTGTTAAAGTTATGATGCTGTGTGCTGTAAAAATGATTTGATTTCTCTCT 900
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Db 841 ATTCTGTTAAAGTTATGATGCTGTGTGCTGTAAAAATGATTTGATTTCTCTCT 900
QY 901 CCAGACTCTGAGGATTCCTGCTCTGTACATAAATGTAAGTTAAATATGATTCAGTA 960
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Db 901 CCAGACTCTGAGGATTCCTGCTCTGTACATAAATGTAAGTTAAATATGATTCAGTA 960
QY 961 AAATGATGCAATGATTAATTTCTCTGTGTTAAAGCTGTAATCATATGATTCATG 1020
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Db 961 AAATGATGCAATGATTAATTTCTCTGTGTTAAAGCTGTAATCATATGATTCATG 1020
QY 1021 GAACATTTATTTCTATATTTTGTGTTTCAATAGGGTGGCTGTGAATGCTGACTAT 1080
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Db 1021 GAACATTTATTTCTATATTTTGTGTTTCAATAGGGTGGCTGTGAATGCTGACTAT 1080
QY 1081 AAATATGAGGAATGATTTTATCAAGTAGAATCCTTTAAACAAGTGAATAGGCTCTT 1140
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Db 1081 AAATATGAGGAATGATTTTATCAAGTAGAATCCTTTAAACAAGTGAATAGGCTCTT 1140
QY 1141 GGTGATGTTGTTAGTTGCTTCCCAAGAGCAATGTCAGAGATTTCTTCCAGAGAGAT 1200
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Db 1141 GGTGATGTTGTTAGTTGCTTCCCAAGAGCAATGTCAGAGATTTCTTCCAGAGAGAT 1200
QY 1201 TCCACACTGAGTAGAGGTGCGTGTAGTCTCGCTGCACTTCTGACTCTTCTCACTCTA 1260
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Db	1201	TCCACACTGAGTGAGAGGTCGGTGCCTAGTCTCCGTGCAGCTTCCTGACTCTTCTCTCACTCTA	1260
QY	1261	ACGTGTTTCTGAAAGTATTAGCAACTCAGAAATTATATTTTGAACCATGATCAGTAGAC	1320
Db	1261	ACGTGTTTCTGAAAGTATTAGCAACTCAGAAATTATATTTTGAACCATGATCAGTAGAC	1320
QY	1321	ATTAAATATATTAACAAATGCCCTATATTAATTAATTCGCACTACTTAATATTAATGACT	1380
Db	1321	ATTAAATATATTAACAAATGCCCTATATTAATTAATTCGCACTACTTAATATTAATGACT	1380
QY	1381	ATATGATGGTGTGTATGCATTTGAATATGCTGTGTCATATTAATAATGTAAAAATATATAGTT	1440
Db	1381	ATATGATGGTGTGTATGCATTTGAATATGCTGTGTCATATTAATAATGTAAAAATATATAGTT	1440
QY	1441	TATTAGTCTAAATAGAAATAAACTACCAGCTAGAACTGTAGAACAACATTGATATGAGTT	1500
Db	1441	TATTAGTCTAAATAGAAATAAACTACCAGCTAGAACTGTAGAACAACATTGATATGAGTT	1500
QY	1501	TAATGTATATGCATTACACTTCCAAAACACTTTTTCAGTTACATAATTAAGTTATAT	1560
Db	1501	TAATGTATATGCATTACACTTCCAAAACACTTTTTCAGTTACATAATTAAGTTATAT	1560
QY	1561	CCTTTATAAAACTCCTCAGTAATCATATAGCTTCATCTACTTTTGAAAAATTTATCTT	1620
Db	1561	CCTTTATAAAACTCCTCAGTAATCATATAGCTTCATCTACTTTTGAAAAATTTATCTT	1620
QY	1621	AATATGTGTGTTGTGTGCTTAGAAAAACAACAACAACTCTTTGGAGAAGGAACTCA	1680
Db	1621	AATATGTGTGTTGTGTGCTTAGAAAAACAACAACAACTCTTTGGAGAAGGAACTCA	1680
QY	1681	TGTAATATACCACAAACAAAGCCTAACTTTGTGGACCACAAATTTGTTTAATATATTTT	1740
Db	1681	TGTAATATACCACAAACAAAGCCTAACTTTGTGGACCACAAATTTGTTTAATATATTTT	1740
QY	1741	TTAATTGATGAATTAANAAGTATATATTTATTTGTGTACATATGATGTTTGAAGTAT	1800
Db	1741	TTAATTGATGAATTAANAAGTATATATTTATTTGTGTACATATGATGTTTGAAGTAT	1800
QY	1801	GTATACATTGCAGAAATGGACAATGGACCAAATTTTATACCTTGCTTGATTAATTGCAT	1860
Db	1801	GTATACATTGCAGAAATGGACAATGGACCAAATTTTATACCTTGCTTGATTAATTGCAT	1860
QY	1861	TTTAAAAATTTTCCTCATTTAGCACCAACTGTGCACGTGAAGAAATCTTTCAGGGAATAGG	1920
Db	1861	TTTAAAAATTTTCCTCATTTAGCACCAACTGTGCACGTGAAGAAATCTTTCAGGGAATAGG	1920
QY	1921	CACACTGGAGAGTCAAACTGTGCAAGGGGTACTGTGAAAAAGACTATTCAAAAACTGTG	1980
Db	1921	CACACTGGAGAGTCAAACTGTGCAAGGGGTACTGTGAAAAAGACTATTCAAAAACTGTG	1980
QY	1981	CTTAATAAAGAAATACATTGACGGGCCAAAAAGTAAGTTACACACATTCAATGGAAGCTAT	2040
Db	1981	CTTAATAAAGAAATACATTGACGGGCCAAAAAGTAAGTTACACACATTCAATGGAAGCTAT	2040
QY	2041	ATTTGTCTCGCTGTGCCTATTTCTATGGAATTGCAGTTTCCCTGTATACCTATTTGTCA	2100
Db	2041	ATTTGTCTCGCTGTGCCTATTTCTATGGAATTGCAGTTTCCCTGTATACCTATTTGTCA	2100
QY	2101	TTTTTCTTTTTCACAGAAAAAAGTGTGGAGAAGAAAGACGGAGATTAACCAATTCTAG	2160
Db	2101	TTTTTCTTTTTCACAGAAAAAAGTGTGGAGAAGAAAGACGGAGATTAACCAATTCTAG	2160
QY	2161	ACTACCTGCAAGAGTTTCTGTGTATGAAACCGGAGTGAATATAGAAAGTTGAGACT	2220
Db	2161	ACTACCTGCAAGAGTTTCTGTGTATGAAACCGGAGTGAATATAGAAAGTTGAGACT	2220
QY	2221	AAACTGTTTGTTCAGCCAAAGATTTTGGAGGAGAAGACATTTTACTGCAGTGAGAA	2280
Db	2221	AAACTGTTTGTTCAGCCAAAGATTTTGGAGGAGAAGACATTTTACTGCAGTGAGAA	2280
QY	2281	GAGGGCCAAGAAAGAGTCAAGGCTTAATTTTCAATTAATTTAACTTCAGAGGGAAAGTA	2340
Db	2281	GAGGGCCAAGAAAGAGTCAAGGCTTAATTTTCAATTAATTTAACTTCAGAGGGAAAGTA	2340

QY	2341	AATATTTCAGGCATACTGACACTTTGGCCAGAAAGCATAAATTTCTTAAATAATATATTTTCAG	2400
Db	2341	AATATTTCAGGCATACTGACACTTTGGCCAGAAAGCATAAATTTCTTAAATAATATATTTTCAG	2400
QY	2401	ATATCAGAATCATTTGAAGTATTTTCCCTCCAGGCCAAAAATGATATACTTTTTCCTATTTTA	2460
Db	2401	ATATCAGAATCATTTGAAGTATTTTCCCTCCAGGCCAAAAATGATATACTTTTTCCTATTTTA	2460
QY	2461	ACTTAACATTTCTGTAAAAATGCTCTGTTAACTTAATATGATTTATGAAATGGTTAAGAAATTT	2520
Db	2461	ACTTAACATTTCTGTAAAAATGCTCTGTTAACTTAATATGATTTATGAAATGGTTAAGAAATTT	2520
QY	2521	GGTAAATTAGTATTTATTTAATGTTATGTTGTGTCTAATAAAAAACAATAATAGACAAC	2580
Db	2521	GGTAAATTAGTATTTATTTAATGTTATGTTGTGTCTAATAAAAAACAATAATAGACAAC	2580
QY	2581	TTCAATTTGCTGCTGGCCTCTGTCCTTAGCAATTTGAAGTTAGCACAGTCCATTTGAGTAC	2640
Db	2581	TTCAATTTGCTGCTGGCCTCTGTCCTTAGCAATTTGAAGTTAGCACAGTCCATTTGAGTAC	2640
QY	2641	ATGCCCAGTTTGGAGGAAGGGTCTGAGCACATGTGGCTGAGCATCCCATTTTCTCTGGAG	2700
Db	2641	ATGCCCAGTTTGGAGGAAGGGTCTGAGCACATGTGGCTGAGCATCCCATTTTCTCTGGAG	2700
QY	2701	AAGTCTCAAGGTTGCAAGGCACACACCAGAGGTGGAAGTGAATCTTAGCAGAGACTTATGCGGGA	2760
Db	2701	AAGTCTCAAGGTTGCAAGGCACACACCAGAGGTGGAAGTGAATCTTAGCAGAGACTTATGCGGGA	2760
QY	2761	TGTGGGGAGCAGGAGACACAGGCAGAGGTGAACCTGGTTTCTCTCTACAGTATATCCAG	2820
Db	2761	TGTGGGGAGCAGGAGACACAGGCAGAGGTGAACCTGGTTTCTCTCTACAGTATATCCAG	2820
QY	2821	AACCTGGGATGTCGAAGGGTAAATGTTAGGGAATTAATGAATGAATGTCTGTTCCACA	2880
Db	2821	AACCTGGGATGTCGAAGGGTAAATGTTAGGGAATTAATGAATGAATGTCTGTTCCACA	2880
QY	2881	TGATTTGTAGAACTAAATATGAGTTGTAAGCTCCCCCTGGAAGAGGAGTGTGAACCTGTAA	2940
Db	2881	TGATTTGTAGAACTAAATATGAGTTGTAAGCTCCCCCTGGAAGAGGAGTGTGAACCTGTAA	2940
QY	2941	CTAGGTTCTCTGCCCCAGCCTGTGAGAAGAAATTTGGCAGATCATCTCATTTGCCAGATAGAG	3000
Db	2941	CTAGGTTCTCTGCCCCAGCCTGTGAGAAGAAATTTGGCAGATCATCTCATTTGCCAGATAGAG	3000
QY	3001	AGGAAGCCAGAAACCCTCTCTGCCCCAAGGCTGCAGGGGTTCTTACCACCTGCACCTGCAC	3060
Db	3001	AGGAAGCCAGAAACCCTCTCTGCCCCAAGGCTGCAGGGGTTCTTACCACCTGCACCTGCAC	3060
QY	3061	CATAACAAAAGACAGAGAGACATGTAGGGCAGTCCCATTTGAAGAAGACTGATTCGGTA	3120
Db	3061	CATAACAAAAGACAGAGAGACATGTAGGGCAGTCCCATTTGAAGAAGACTGATTCGGTA	3120
QY	3121	TTCCCGGGGACAGGACACACAGGCCGACACAACATTCATTCCTGCTTATGGCTATCA	3180
Db	3121	TTCCCGGGGACAGGACACACAGGCCGACACAACATTCATTCCTGCTTATGGCTATCA	3180
QY	3181	GTAGCATCACTAGAGATTTCTCTGTTTGAGAAAACTTCTCTCAAGATCC 3230	
Db	3181	GTAGCATCACTAGAGATTTCTCTGTTTGAGAAAACTTCTCTCAAGATCC 3230	

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RESULT 3
US-09-079-839-2
; Sequence 2, Application US/09079839
; Patent No. 6048726
; GENERAL INFORMATION:
; APPLICANT: Weltman, Joel K.
; APPLICANT: Karim, Aftab S.
; TITLE OF INVENTION: INHIBITION OF EOSINOPHILIC INFLAMMATION
; FILE REFERENCE: 09998/002001
; CURRENT APPLICATION NUMBER: US/09/079, 839
; CURRENT FILING DATE: 1998-05-15

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: TITLE OF INVENTION: IL-5 TRANSGENIC MOUSE
: NUMBER OF SEQUENCES: 5
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Schwegman, Lundberg, Woessner & Kluth, P. A.
: STREET: P. O. Box 2938
: CITY: Minneapolis
: STATE: MN
: COUNTRY: USA
: ZIP: 55402
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette
: COMPUTER: IBM Compatible
: OPERATING SYSTEM: DOS
: SOFTWARE: FastSeq Version 2.0
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/629,643A
: FILING DATE:
: CLASSIFICATION: 800
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/629,643
: FILING DATE: 09-APR-1996
: ATTORNEY/AGENT INFORMATION:
: NAME: Viksnins, Ann S
: REGISTRATION NUMBER: 37,748
: REFERENCE/DOCKET NUMBER: 150.167W01
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 612-359-3260
: TELEFAX: 612-359-3263
:
: TELEX:
:
: INFORMATION FOR SEQ ID NO: 5:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 6727 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: genomic DNA
: FEATURE:
: NAME/KEY: mat_peptide
: LOCATION: 650..3771
: OTHER INFORMATION: John 650..730, 1560..1592,
: OTHER INFORMATION: 3468..3596, 3676..3771
:
: US-08-629-643A-5

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Db      734 A 734

RESULT 6
US-09-280-799-1
; Sequence 1, Application US/09280799
; Patent No. 6136603
; GENERAL INFORMATION:
; APPLICANT: Dean, Nicholas M.
; APPLICANT: Karras, James G
; APPLICANT: McKay, Robert
; TITLE OF INVENTION: ANTISENSE MODULATION OF INTERLEUKIN-5 SIGNAL
; FILE REFERENCE: ISPH-0340
; CURRENT APPLICATION NUMBER: US/09/280,799
; CURRENT FILING DATE: 1999-03-26
; NUMBER OF SEQ ID NOS: 208
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 6727
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-280-799-1

Query Match          5.0%; Score 161.8; DB 3; Length 6727;
Best Local Similarity 71.5%; Pred. No. 1.2e-28;
Matches 258; Conservative 0; Mismatches 92; Indels 11; Gaps 3;

QY    343 TTTTATTATTAAGATAAAGTAATTTATTTTTTAAGATATAAGGCATTGGAACAT 402
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Db    382 TATTAAGAGCAAAAAAAAAAAATGCATTTTGTTGAAGACCAGGGCCTGGAACCC 441

QY    403 TTACTTTCAGCATATGCCATTTAGGCATTCTCTATCTGATGTGTAACAATTATTCATT 462
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Db    442 TGAGTTTCAGGACTCGCCCTTATTAGGTGTCCTCTATCTGATGTGTAACAATTATTCATT 501

QY    463 TCCTCAAAGACAGACAATAATTGACTGGGGACGAGTCCTGTACTATGCACCTTCTTGG 522
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Db    502 TCCTC--AGAGAGAATAAATTGCTTGGGGATTGGCCCTGCTCTGCGCTCTCTTGG 559

QY    523 CCAAAGGCAACGACAGAACGTTTCAGAGCCATG--AGATGCTTTCGATTGAGTTTG 579
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Db    560 CTGAAGGCCAGCGCTGAAGACTTCAGAGTCATGAGAAGATGCTTCTGCACCTGAGTGT 619

QY    580 CTAGCTCTTGAGCTGCGCTAGCTGTATGCCATCCCACAGAAAATCCACAGTGCATTG 639
      || ||||| | ||||| || ||||| ||||| ||||| ||||| ||||| ||||| |||||
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QY    640 GTGAAGAGAGACCTTGGCAGCTGTTTCTACTCATCGAAGCTGTGCTGATAGCCAATGAGGTA 699
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Db    674 GTGAAGAGAGACCTTGCACACAGCTGTCCGCTCACCAGAGCTGTGTGACAAAGCAATGAGGTA 733

QY    700 A 700
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Db    734 A 734

RESULT 7
US-09-155-884-5
; Sequence 5, Application US/09155884
; Patent No. 6215040
; GENERAL INFORMATION:
; APPLICANT: James J. Lee et al.
; TITLE OF INVENTION: IL-5 TRANSGENIC MOUSE
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Schwegman, Lundberg, Woessner & Kluth, P. A.
; STREET: P. O. Box 2938
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402
; COMPUTER READABLE FORM:
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MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/155,884
FILING DATE: Unknown
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US97/05932
FILING DATE: 09-APR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Viksnins, Ann S
REGISTRATION NUMBER: 37,748
REFERENCE/DOCKET NUMBER: 150.167US2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-359-3260
TELEFAX: 612-339-3061
TELEX:
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 6727 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Genomic DNA
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 650...3771
OTHER INFORMATION: Join 650..730, 1560..1592,
OTHER INFORMATION: 3468..3596, 3676..3771
US-09-155-884-5
Query Match 5.0%; Score 161.8; DB 4; Length 6727;
Best Local Similarity 71.5%; Pred. No. 1.2e-28;
Matches 258; Conservative 0; Mismatches 92; Indels 11; Gaps 3;
QY 343 TTTTATTATTAAGATAAAGTAAATTTATTTTAAAGATATAGGATGGAACAT 402
DB 382 TATTAAAGAGCAAAAAAATGATTTGTTGAAGACCAGGCACTGAAACCC 441
QY 403 TTAGTTTACGATATGCCATTATTAGGCAATCTATCTGATTTAGAAATTTATTCAT 462
DB 442 TGAGTTTACGACTCGCTTTATTAGTGTCTCTATCTGATTTAGCAATTTATTCAT 501
QY 463 TCCTCAAGACAGACAATAATTGACTGGGAGCAGCTTGTACTATGCACTTTCTTTG 522
DB 502 TCCTC--AGAGAGAGATAAATGCTTGGGAGATCGCCCTGCTCGCCTCTCTCTT 559
QY 523 CCAAAGGCAACGACAGATTTTCAGAGCCATG---AGGATGCTTCTGCAATTTGAGTTG 579
DB 560 CTGAAGGCGCAGCTGAGACTTCAGAGTCAAGAGGATGCTTCTGCACTTTGAGTTG 619
QY 580 CTAGCTCTTGAGCTGCTTACGCTGATGATGCCATCCCAAGAAATTTCCACAGTGCATTG 639
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DB 674 GTGAAGAGAGACCTTGAGACAGCTGTCCGCTCACCAGCTCTGTTGACAAGCAATGAGGTA 733
QY 700 A 700
DB 734 A 734
RESULT 8
US-09-180-864-1
Sequence 1, Application US/09180864
Patent No. 6465616
GENERAL INFORMATION:
APPLICANT: Lopez, Angel
APPLICANT: Vadas, Matthew

APPLICANT: Shannon, Frances
APPLICANT: Bastiras, Stan
APPLICANT: Hey, Allan W
TITLE OF INVENTION: AN INTERLEUKIN-5 ANTAGONIST
FILE REFERENCE: 99722
CURRENT APPLICATION NUMBER: US/09/180,864
CURRENT FILING DATE: 1999-04-12
PRIOR APPLICATION NUMBER: 08/591,438
PRIOR FILING DATE: 1994-07-28
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 1
LENGTH: 377
TYPE: DNA
ORGANISM: nucleotide sequence encoding modified IL-5
FEATURE:
NAME/KEY: CDS
LOCATION: (4)..(366)
US-09-180-864-1
Query Match 3.9%; Score 126.8; DB 4; Length 377;
Best Local Similarity 86.4%; Pred. No. 6.8e-21;
Matches 140; Conservative 0; Mismatches 22; Indels 0; Gaps 0;
QY 1849 GATTATTGCAATTTTAAATTTTCCCTCATTTAGCACCACTGTGCACGAAATCTT 1908
DB 108 GACTTGAGGATTCCTCTGTTCTGATCATATAAATCACCACACTGTGCACGAAATCTT 167
QY 1909 TCAGGGAATAGGACACACTGAGAGTCAAACTGTGCAAGGGGTACTGTGAAAGACTATT 1968
DB 168 TCAGGGAATAGGACACACTGAGAGTCAAACTGTGCAAGGGGTACTGTGAAAGACTATT 227
QY 1969 CAAAACTGTCTTAAATAAAGAAATACATTGACGGCCAAA 2010
DB 228 CAAAACTGTCTTAAATAAAGAAATACATTGACGGCCAAA 269
RESULT 9
US-08-629-643A-4
Sequence 4, Application US/08629643A
Patent No. 6025539
GENERAL INFORMATION:
APPLICANT: Lee, J. L.
APPLICANT: Lee, N. A.
TITLE OF INVENTION: IL-5 TRANSGENIC MOUSE
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Schwegman, Lundberg, Woessner & Kluth, P. A.
STREET: P. O. Box 2938
CITY: Minneapolis
STATE: MN
COUNTRY: USA
ZIP: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/629,643A
FILING DATE:
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/629,643
FILING DATE: 09-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Viksnins, Ann S
REGISTRATION NUMBER: 37,748
REFERENCE/DOCKET NUMBER: 150.167W01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-359-3260
TELEFAX: 612-359-3263
TELEX:

MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-487-826B-13

Query Match 1.7%; Score 54.6; DB 2; Length 19124;
Best Local Similarity 46.1%; Pred. No. 0.0028;
Matches 257; Conservative 0; Mismatches 294; Indels 6; Gaps 2;

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QY 1729 AATAATTTATTTTAAATGATGAATTAAGATATATATATATATATATATATATATAT 1788
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DB 6463 ATTTATCATTTTATTTTGTGATGCTATATATATATATATATATATATATATATATAC 6522
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Search completed: April 24, 2003, 03:52:24
Job time : 464 secs

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GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: April 23, 2003, 22:59:42 ; Search time 335 Seconds

(without alignments)
10491.510 Million cell updates/sec

Title: US-09-800-629A-78
Perfect score: 3230
Sequence: 1 atcctaatacaagaccacagtl.....aaaacttctcaagatcc 3230

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 709820 seqs, 544064369 residues

Total number of hits satisfying chosen parameters: 1419640

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications_NA:*

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- 2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
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- 14: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	600.6	18.6	1658	10	US-09-755-633-18
3	589.6	18.3	1658	10	US-09-755-633-19
4	205	6.3	671	10	US-09-755-633-21
5	161.8	5.0	6727	10	US-09-800-629A-1
6	152.4	4.7	610	10	US-09-755-633-4
7	152.4	4.7	610	10	US-09-755-633-6
8	99.4	3.1	402	10	US-09-755-633-7
9	99.4	3.1	402	10	US-09-755-633-8
10	90.2	2.8	345	10	US-09-755-633-9
11	90.2	2.8	345	10	US-09-755-633-11
12	61	1.9	32187	9	US-10-092-154-1550
13	61	1.9	32187	10	US-09-764-847-1550
14	61	1.9	32193	9	US-10-092-154-1549
15	61	1.9	32193	10	US-09-764-847-1549
16	59.4	1.8	99916	10	US-09-816-095-3
17	57.4	1.8	640681	10	US-09-790-988-1
18	57.4	1.8	640681	10	US-09-790-988-1
19	57	1.8	513509	9	US-09-754-853A-4

C	20	55.4	1.7	5917	9	US-10-087-464-9	Sequence 9, Appli
C	21	55	1.7	302250	10	US-09-962-832-154	Sequence 154, App
C	22	54.6	1.7	513509	9	US-09-754-853A-4	Sequence 4, Appli
C	23	54	1.7	397658	10	US-09-813-320-3	Sequence 3, Appli
C	24	53.6	1.7	335913	9	US-09-754-853A-2	Sequence 2, Appli
C	25	53.6	1.7	335913	9	US-09-754-853A-3	Sequence 3, Appli
C	26	52	1.6	143068	10	US-09-967-768A-316	Sequence 316, App
C	27	51.4	1.6	2000	9	US-09-938-842A-4305	Sequence 4305, App
C	28	50.4	1.6	172637	10	US-09-805-458A-3	Sequence 3, Appli
C	29	50.2	1.6	1367	9	US-09-938-842A-4999	Sequence 4999, App
C	30	50.2	1.6	1376	9	US-10-011-445-21	Sequence 21, Appli
C	31	50	1.5	1864	9	US-10-105-481-4	Sequence 4, Appli
C	32	49.8	1.5	1803	10	US-09-822-830A-306	Sequence 306, App
C	33	49.8	1.5	197496	9	US-09-877-177-10	Sequence 10, Appli
C	34	49.6	1.5	464	9	US-10-046-935-47	Sequence 47, Appli
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C	37	49.2	1.5	2000	9	US-09-938-842A-3817	Sequence 3817, App
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C	39	49	1.5	12003	10	US-09-764-877-3976	Sequence 3976, App
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C	41	48.6	1.5	147309	10	US-09-742-312-3	Sequence 3, Appli
C	42	48.4	1.5	15577	9	US-10-158-160A-8	Sequence 8, Appli
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C	44	48.4	1.5	302250	10	US-09-962-832-154	Sequence 154, App
C	45	48.4	1.5	684973	10	US-09-263-959-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-09-800-629A-78
Sequence 78, Application US/09800629A
Patent No. US20020128216A1
GENERAL INFORMATION:
APPLICANT: Dean, Nicholas M.
APPLICANT: Karras, James G
APPLICANT: McKay, Robert
APPLICANT: Manoharan, Muthiah
TITLE OF INVENTION: ANTISENSE MODULATION OF INTERLEUKIN-5 SIGNAL
FILE REFERENCE: ISPH-0537
CURRENT APPLICATION NUMBER: US/09/800, 629A
CURRENT FILING DATE: 2001-03-07
PRIOR APPLICATION NUMBER: PCT/US00/07318
PRIOR FILING DATE: 2000-03-17
PRIOR APPLICATION NUMBER: 09/280, 799
NUMBER OF SEQ ID NOS: 210
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 78
LENGTH: 3230
TYPE: DNA
ORGANISM: Homo sapiens
US-09-800-629A-78

Query Match 100.0%; Score 3230; DB 10; Length 3230;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1741 TTAATGATGATTTAAAAAGTATATATTTATTTGTTGACATAATGATGTTTGAAGTAT 1800
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| | | | |
Db 1801 GTATACATTTGCAAGATGGAATGGAACCAAAATTTTATACCTGCTGATTAATTTGCAT 1860
QY 1861 TTTAAAAATTTTCTCATTTAGCACCACTGTGACCTGAAGAAATCTTTCAGGGAATAGG 1920
| | | | |
Db 1861 TTTAAAAATTTTCTCATTTAGCACCACTGTGACCTGAAGAAATCTTTCAGGGAATAGG 1920
QY 1921 CACACTGAGAGTCAAACTGTGCAAGGGGTACTGTGAAAGACTATTCAAAAACCTTCTC 1980
| | | | |
Db 1921 CACACTGAGAGTCAAACTGTGCAAGGGGTACTGTGAAAGACTATTCAAAAACCTTCTC 1980
QY 1981 CTTAATAAAGAAATACATTTGACGGGCCAAAAAGTAAGTTACACACATTCATGGAAGCTAT 2040
| | | | |
Db 1981 CTTAATAAAGAAATACATTTGACGGGCCAAAAAGTAAGTTACACACATTCATGGAAGCTAT 2040
QY 2041 ATTTGCTGCTGCTGCTGCTATTTTCTATGGAATTTGACAGTTTCTGTAATACCTATTTGCA 2100
| | | | |
Db 2041 ATTTGCTGCTGCTGCTGCTATTTTCTATGGAATTTGACAGTTTCTGTAATACCTATTTGCA 2100
QY 2101 TTTTCTTTTTCACAGAAAAAGTGTGAGAGAAAGACGAGAGTAAACCAATTCCTAG 2160
| | | | |
Db 2101 TTTTCTTTTTCACAGAAAAAGTGTGAGAGAAAGACGAGAGTAAACCAATTCCTAG 2160
QY 2161 ACTACCTGCAAGAGTTTCTTGTGTAATGAACACCGAGTGGAATTAAGAAAGTGAAGCT 2220
| | | | |
Db 2161 ACTACCTGCAAGAGTTTCTTGTGTAATGAACACCGAGTGGAATTAAGAAAGTGAAGCT 2220
QY 2221 AAACCTGTTGTTGCAAGCAAAAGATTTTGAGAGAGAAAGACATTTACTGAGTGAGAT 2280
| | | | |
Db 2221 AAACCTGTTGTTGCAAGCAAAAGATTTTGAGAGAGAAAGACATTTACTGAGTGAGAT 2280
QY 2281 GAGGGCCAAAGAGAGTCAAGGCTTAATTTTCAATATATTAATTTCAAGAGGAAAGTA 2340
| | | | |
Db 2281 GAGGGCCAAAGAGAGTCAAGGCTTAATTTTCAATATATTAATTTCAAGAGGAAAGTA 2340
QY 2341 AATATTTCAAGCAATCTGACACTTTGCGAGAAAGCATAAATTTCTTAAATATATTTGAG 2400
| | | | |

QY	1284	ACACGAAATTATATTTTGAACCATGATCAGTAGACATTTAAATATATAACAAATGCC-	1342
Db	769	ACTTGGGGTTATATTTTGAATATATGCTCAGTAGACATGAATAATATACAGTGAAGTCC	828
QY	1343	--CTATATTAAATTAATTCGCATCTTAAATAATTATGACTATATGATGCTGTATGCAT	1400
Db	829	ATATTAAATAGTCACCTCCACATATTTAAATGATTTTAACTCTAATGGAATCATATACAT	888
QY	1401	TGAATAT---GCCGTGCATATTTAAATGTAAATATAT-AGTTTATAGTCTAAATAGA	1456
Db	889	CTGCAGTATGTCATGGTCATATTAATAATGTTAAAAATGTGATATCATTAGTCTAAATAGA	948
QY	1457	ATAAACTACCACTAGAACTGTAGAACAACAT--TGATATGAGTTTATGTATATGC-	1513
Db	949	ATAAAATTACCACTAGAACTATACGAGGAATCTGAGGTGAGGTAATCAGTAAGCA	1008
QY	1514	-----ATTACACTTCCAAACAATTTTTTCCAGTTACATATTAAGTTATATCCTTTATA	1568
Db	1009	GTTGTATATATACCTCGTAAGCATTTATTTTCATTTAATCATTTTCATTTATATCATTTGTA	1068
QY	1569	AAACTCCTCAGTAATCATATTAAGCTTTCATCTACTTTTGAATAATTTATCTTAATATGTG	1628
Db	1069	ACACTTCTCAGTAATTAATTAACAATCATTTAC-TTATGTGTAATTAATAGCTTAGTAATAG	1127
QY	1629	GTTGTTTGTGCTTAGAAA-----ACAACAATAAACTCTTTGGAGAAGGGAACCTCATGTA	1684
Db	1128	GTGTTTCCACCTGGAAAGACACAAGTAAAAACCTCTTGGAGAAGGGAACCTGTGTA	1187
QY	1685	AATACCACAAAACAAAGCCTAATTTGTGACCAAAAATGTTTTAATATATTTTAA	1744
Db	1188	AACCCACAAAACAAAGCTTAACCTTTT-----	1214
QY	1745	TTGATGAATTAAGATATATATTTATTTGTGTACAAATATGATGTTTGAAGTATGTAT	1804
Db	1215	-----	1214
QY	1805	ACATTGCAGAATGACAAATGGACCAAAATTTTATACCTGTCTTGATTAATTGCA-TTTT	1863
Db	1215	-----TGACCAAAATTTTATGCTGTTTGTGATGAATTAATTTT	1256
QY	1864	AAAAATTTTCCCTCATTTTACACCAACTGTGCACCTGACAGAAATCTTTCAGGGAATAGCCAC	1923
Db	1257	TAAATCTCTCCATTTTACCACTGTGCATTTAAGAAATTTTTCAGGGAATAGCACAC	1316
QY	1924	ACTGGAGAGTCAAACTGTGCAGAAGGGGACTGTGGAAGAATATTCMAAAACTGTCTT	1983
Db	1317	ATTGAAGAACCACAACTGCCACCGGGAGGCTGTGATAACTATTTCCAAAACCTGTCTT	1376
QY	1984	AATAAAGAATATCATTTGACGGCCAAAAGTAAGTTACACACATTCATGGAAGCTATATT	2043
Db	1377	AATAAAGAACACATATAGAGCGCCAAAAGTAAGTTAAGACATTTGGCAAAACTTAAAGT	1436
QY	2044	TGTCCTGGCTG-----TGCTATTTCTATGGAATTGACAGTTTCTCTG	2085
Db	1437	ATATTTGTCTGACTGTGCCCTGTTTTTTTTTTTTTTTAAAGAAATTGACAGTTTCTTA	1496
QY	2086	TAAATCCTATTTGTCAATTTTCTTTTTCACAGAAAAAGTGTGAGAAGAAAGACGAGAG	2145
Db	1497	CAATATCT-----CCTCTGTTCTTTAAACAGAAAAGGTGTGCAGAGAAAGATGAGAG	1550
QY	2146	TAAACCAATTCCTAGACTACCTGCAGAGAGTTCTTGGTGTATATGAACACCGAGTGCATTA	2205
Db	1551	TGACAAAGTTCCTAGACTACCTGCAGAGATTTCTTGGTGTATTAACACCCGAGTGACAC	1610
QY	2206	TAGAAAGTTGAGACTTAAACTGTGTTTGTGTGCAGCCAAAGATTTTGGAG	2252
Db	1611	CGGAAAGTTGAGAACAAACCGGCTTATTTGTAGTGAAGATTTTGGAG	1657

```

: Patent No. US20020127200A1
:
: GENERAL INFORMATION:
:
: APPLICANT: Yang, Shumin
: APPLICANT: McCall, Catherine A.
: APPLICANT: Weber, Eric R.
:
: TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
: TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF
:
: FILE REFERENCE: IM-2-C1-C1
:
: CURRENT APPLICATION NUMBER: US/09/755,633
:
: CURRENT FILING DATE: 2001-01-05
:
: PRIOR APPLICATION NUMBER: 09/322,409
:
: PRIOR FILING DATE: 1999-05-28
:
: PRIOR APPLICATION NUMBER: 60/087,306
:
: PRIOR FILING DATE: 1998-05-29
:
: NUMBER OF SEQ ID NOS: 21
:
: SOFTWARE: PatentIn Ver. 2.1
:
: SEQ ID NO 19
:
: LENGTH: 1658
:
: TYPE: DNA
:
: ORGANISM: Canis familiaris
:
: US-09-755-633-19

```

Query Match	18.3%	Score 589.6;	DB 10;	Length 1658;
Best Local Similarity	67.4%;	Pred. No. 4.8e-107;		
Matches 1206; Conservative	0;	Mismatches 389;	Indels 193;	Gaps 19;

QY	527	AGCCAAACGCAAGACGTTTCAGAGCCATGAGGATGCTTCTGCATTGTGAGTTTGCTAGCTC	586
Db	1658	AGCCAAACACTGAACATTTTCAGAGCTATGACAATGCTTCTGAAATTGGATTGCTAGCTC	1599
QY	587	TTGGAGCTGCCCTACGTTGTAAGCATCCCCACAGAAAATCCCACAAGTGCATTTGCTGAAG	646
Db	1598	TTGGGCTGCCCTATGTTTCTGCCCTTTCGCTGTAGAATAATCCCATGAATAGACTGGTGCGAG	1539
QY	647	AGACCTTGGCACTGCTTTCCTACTCATCGAAGCTCTGCTGATAGCCAATGAGTAATTTCT	706
Db	1538	AGACCTTGACACTGCTCTCCACATCATCGAAGCTTGCTGATAGCGCATGGGTAATTTCT	1479
QY	707	TTATGATTCCTACAGTCTGTAAAGTGCATAGGTAATTCATTTGTGATGGTTCTTACTAT	766
Db	1478	TTTTGATTCCTACAGTCTTTAAATGCATGGGTAATTTGGTGGTGCTAGTT-----	1425
QY	767	ATATAGAGATCTGTTATAATTAATAGATTCTGA--GCACATTAGTACATGGGTGATAAC	824
Db	1424	-TTTAAAGATTCATTATCATTAATGAAGTAATGAGTGTATAATATTAATTAATGGGTACC	1366
QY	825	TACATCACCAAGCAAACATTCGTAAAAAGTTANGAATGCTGTGCTGTAAAAATGATT	884
Db	1365	CATGTTACTCAGAAGATTATTAATAAGTTATGAACCTTACAATACATTAATAAATGAAT	1306
QY	885	G-TATTTCTCTTCCCTCTCCAGACTCTGAGGATTCCCTGTCCTGTACATAAAAATGTAAGT	943
Db	1305	GTTGTTCTCTTCTTTTTCAGAACCTGATGATTCCCTACTCCTGAAAAATAAAAATGTAAGT	1246
QY	944	TAAATTAATGATTCAGTAAATAATGATGGCATGAAATAAGTAAATTTCCCTGTTTAAAGCTGTAA	1003
Db	1245	TAAATTAATGATTTGATTAATAATGAATACATGAATCAG---TTTCATATTTTAAAGCTATAA	1190
QY	1004	ATCATTAGTTAATCATTTGGAAGTAATTTAATTTTCTAATTTTGTTCATATATGGTGCGCTG	1063
Db	1189	AGTATCAGTTAACAATTGGATGATTTAATTTTATCTAATTTTGTTTATATGTGTGCGGANG	1130
QY	1064	TGAATGCTCTACTTATATAATATGAGGAATGACTT-----TTATCAAGT	1108
Db	1129	TAAAT-TATGTGCTTATGAATATTTAGGAATGCTGTAGGAATGGCTCTACAATATTAACT	1071
QY	1109	AGAATCCTTTAAACAAGTGAATTAGGCTCTTTGSHGATGTTGTAGTTTGCTTCCCAA	1168
Db	1070	AGAATTCATTTAAGCAAGTGAATCAGCCCTTTTGTGATGTTGTACAGTTCTCCATCTCAA	1011
QY	1169	GAGCATCGTGTGAGG-ATTTCCTTCCAGAGGATTCACACTGAGTGCAGAGGTGCGTCTA	1227
Db	1010	GAGCTCTGTCGAGGCAATCTTTCCAAAAGAAATTCATATTGGGTGCAGAGATACCTTCCTA	951

QY	1228	GTCTCCGTCGAGTTCGAC-----TCTTTCCTACCTCTAACGCTGTTTCTGAAAGTATAGC	1282
Db	950	GGCTCCATTCACCTCTGTCGTTGGCTTTCCTCACCTCAACGTTTTTCTGAAAGTACTAGC	891
QY	1283	AACTCAGAATTATATTTTGAACCATGATCAGTAGACATTTAAATATATTAACAAATGCC	1342
Db	890	AACTTGGGGTATATTTTGTAGAAATTATGCTCAGTAGACATGAAAAATATACAGTAGAAGTCC	831
QY	1343	--CTATATTAAATAATCTCTGCATACCTTAATAATAATGACTATATGATGGTGTATGCA	1399
Db	830	TATATTAAATAGTCACCTCCACATATTTAAATGATTTTAACTCTAATGGAATCATATACA	771
QY	1400	TTGAATAT--GCCCTGTCATATTTAAATGTAAAAATATAT-AGTTTATTTAGTCTAAATAG	1455
Db	770	TCTGAGTATGTGATGTCATATTTAAATGTTAAAAATGTGATATCATTAGTCTAAATAG	711
QY	1456	AATAAACTACCACTAGAACTGTAGAAACACAT--TGATATGAGTTTAATGTATATGC	1513
Db	710	AATAAAATTACCAGCTAGAACTATACGAGGAATTTCTGAGGTGAGTAATCAGTAAGC	651
QY	1514	-----ATTACACTTCCAAAACATTTTTTTCAGTTACATAATTAAGTTATATCCTTAT	1567
Db	650	AGTTGATATTATACCTCGTAAGCATTTATTTTTCATTATCATTTTCAATTATATCATTTGT	591
QY	1568	AAAACTCCTCAGTAATCATATAGCTTCATCTACTTTTGAATAATTTATCTTAATATGT	1627
Db	590	AACACTTCTCAGTAATATATATAACATCATTTTAC-TTATGTTAATTATAGCTTAGATAA	532
QY	1628	GGTGGTTTGTGCTTAGAAA---ACAAACAATAAACTCTTTGAGAGAAGGGAACATCATGT	1683
Db	531	GGTGGTTTCCACCCGGAAGAAGACACAAGTAATAAACTCTTTGGAGAAGGGAACCTGTGT	472
QY	1684	AAATACCACAAAACAAAGCCTAACTTTGTGACCATAAATGTTTAAATAATATATTTTA	1743
Db	471	AAACCCACAAAACAAAGTCTAACTTT-----	445
QY	1744	ATTGATGAATTAATAAGATATATATATTATTGTGTACAATATGATGTTTGAAGTATGTA	1803
Db	444	-----	445
QY	1804	TACATTGCAGATGAGACATGGAACCAATTTTATACCTGTCTTGATTTATTTGCA-TTT	1862
Db	444	-----TGACCAAAATTTTATGCCCTGTTTGTGATGAATTAATTTT	404
QY	1863	TAAAAATTTTCCCTCATTTAGCACCACTGTGCACCTGGAAGAAATCTTTCAGGGAATAGCA	1922
Db	403	TTAAAAATCTTCCCTCATTTAGCACCACTGTGCATTAAGAAGTTTTTTCAGGGTATAGACA	344
QY	1923	CACCTGAGAGTCAAACTGTGCAAGGGGCTACTGTGAAAGACTATTTCAAAAACCTGTCT	1982
Db	343	CATTGAAGAACCAAACTGCCACGCGGAGGCTGTGATTAACCTATTTCCAAAACCTGTCT	284
QY	1983	TAAATAAGAAATACATTTGACGGCCAAAAAGTAAGTTACACACATTCATGGAAGCTATAT	2042
Db	283	TAAATAAGAAACACATAGAGCGCCAAAAAGTAAGTTAAGACATTTGGCAAAAACCTTAAG	224
QY	2043	TTGTCTCGCTG-----TGCCATTTCTATGGAATTGACAGTTTCT	2084
Db	223	TATATTTTGCTGACTCGCCCTGTTTTTTTTTTTTTTTACAGAATTTGACAGTTTCT	164
QY	2085	GTAATACCTATTTCTTTTTCACAGAAAAAGTGTGAGAAGAAGACGAGCA	2144
Db	163	ACAATATCT-----CCCTGCTTCTTTTAAACAGAAAAAGTGTGACAGAGAAGATGAGCA	110
QY	2145	GTAACCAATTTCTAGACTTACCTGCAAGAGTTTCTTGGTGTAAATGAACACCGAGTGTATA	2204
Db	109	GTCACAAAGTTCCTAGACTTACCTGCAAGTATTTCTTGGTGTAAATGAACACCGAGTGTACA	50
QY	2205	ATAGAAAGTTGAGACTAAACTGTTTGTGACAGCCAAAGATTTTGGAG	2252
Db	49	CCGGAAGTTGAGAACAAACCGGCTTATTTGTAGTGAAGATTTTGGAG	2

```

RESULT 4
US-09-755-633-21
; Sequence 21, Application US/09755633
; Patent No. US20020127200A1
; GENERAL INFORMATION:
; APPLICANT: Yang, Shumin
; APPLICANT: McCall, Catherine A.
; APPLICANT: Weber, Eric R.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF
; FILE REFERENCE: IM-2-C1-C1
; CURRENT APPLICATION NUMBER: US/09/755,633
; CURRENT FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: 09/322,409
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/087,306
; PRIOR FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 671
; TYPE: DNA
; ORGANISM: Canis familiaris
US-09-755-633-21

```

	Query Match	Similarity	6.3%;	Score 205;	DB 10;	Length 671;	
	Best Local	Matches	304;	Conservative	0;	Mismatches 100;	Indels 9; Gaps
QY	527	AGGCAACCGCAGAACGTTTCAGAGCCATGAGGATGCTTCTGCATTGTGAGTTTGCTACGCTC					
Db	1	AGGCAACACTGACAACATTTTCAGAGCCTATGAGAAATGCTTCTGAATTGGAGTTTGCTACGCTC					
QY	587	TTCGAGCTGCCCTACGTCGTATGCCATCCCCACAGAAATTTCCCACAAGTGCATTGGTGAAG					
Db	61	TTGGGGCTGCCCTATGTTTCTGCGCTTGCTGTAGAAAAATCCCATGAATAGACTGGTGGCAG					
QY	647	AGACCTTGGCACTGCTTCTCTACTCATCGAACCTCTGCTGANAGCCAATGAGTAATTTCT					
Db	121	AGACCTTGACACTGCTCTCCACACTCATCGAACCTTGGCTGATANAGCGATGGGTAATTTCT					
QY	707	TTATGATTCCTACAGTCTGTAAAGTCATAGGTAATCATTTGTGATGGTTCCTTACTAT					
Db	181	TTTTGATTCCTACAGTCTTTAAAATGCATGGGTAATTGGTGCTGGCTAGTT-----					
QY	767	ATATAGAGATCTGTATAAATAATGAATTCCTGAG-CACATTAGTACATGGGTGATACT					
Db	235	-TTTAAAGATCATTAATCAATGAAGTAATGAGTGTAAATAATATATATGAATGGTAAACC					
QY	826	ACATCACCCAGCAAACATTTCTGTTAAAGTTATGAATGCTGTGTGCTGTAAAAATGATG					
Db	294	ATGTACTCAGAGAATATATATAAAGTTATGAACCTTACATACATTAATAAATGATG					
QY	886	-TATTTCTTCTCTCCAGACTCTGAGGATTCCTGTTCCTGTACATAAAAT					
Db	354	TTGTTCTTCTTTTTCAGAACCTGATGATTCCTACTCTCTGAAAAATAAAAAT					

RESULT 5
US-09-800-629A-1
; Sequence 1, Application US/09800629A
; Patent No. US20020128216A1
; GENERAL INFORMATION:
; APPLICANT: Dean, Nicholas M.
; APPLICANT: Kairas, James G.
; APPLICANT: McKay, Robert
; APPLICANT: Manoharan, Muthiah
; TITLE OF INVENTION: ANTISENSE MODULATION OF INTERLEUKIN-5 SIGNAL
; TITLE OF INVENTION: TRANSDUCTION
; FILE REFERENCE: ISPH-0537
; CURRENT APPLICATION NUMBER: US/09/800,629A
; CURRENT FILING DATE: 2001-03-07


```

; PRIOR APPLICATION NUMBER: PCT/US00/07318
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: 09/280,799
; PRIOR FILING DATE: 1999-03-26
; NUMBER OF SEQ ID NOS: 210
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 6727
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-800-629A-1

```

Query Match	5.0%;	Score 161.8;	DB 10;	Length 6727;
Best Local Similarity	71.5%;	Pred. No. 3.7e-22;		
Matches 258; Conservative	0;	Mismatches 92;	Indels 11;	Gaps 3

[illegible]

RESULT 6
US-09-755-633-4
; Sequence 4, Application US/09755633
; Patent No. US20020127200A1
; GENERAL INFORMATION:

```

APPLICANT: Yang, Shumin
APPLICANT: McCall, Catherine A.
APPLICANT: Weber, Eric R.
TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF
FILE REFERENCE: IM-2-C1-C1
CURRENT APPLICATION NUMBER: US/09/755,633
CURRENT FILING DATE: 2001-01-05
PRIOR APPLICATION NUMBER: 09/322,409
PRIOR FILING DATE: 1999-05-28
PRIOR APPLICATION NUMBER: 60/087,306
PRIOR FILING DATE: 1998-05-29
NUMBER OF SEQ ID NOS: 21
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 4
LENGTH: 610
TYPE: DNA
ORGANISM: Canis familiaris
FEATURE:
NAME/KEY: CDS
LOCATION: (29)..(430)
S-09-755-633-4

```

	Query Match	4.7%	Score 152.4;	DB 10;	Length 610;
	Best Local Similarity	77.3%;	Pred. No. 9e-21;		
Matches	198; Conservative	0;	Mismatches 56;	Indels 2;	Gaps 1;
OY	2114 ACAGAAAAAAGTGTGGAGAAGAAACGAGAGTAACCATTCTTAGACTACCTGCAGA	2173 			
Dd	331 AAAAAAAAAAGCTGTGCAGAGAAAAGATGAGAGTGACAACAAAGTTCCVAGACTACCTGCAAGT	390 			
OY	2174 GTTTCCTGGTGTATGAACACCGAGTGGATAATAGAAAGTTGAGACTAACCTGGTTGTT	2233 			
Dd	391 ATTTCCTGGTGTATTAACACCGAGTGGACACCGAAAGTTGAGAACAAACCGGCTATT	450 			
OY	2234 GCAGCCAAGATTTTGGAGAGACAACGACATTTTACTGCAGTGAAGATGAGGCCCAAAGAA	2293 . 			
Dd	451 GTAAGTGAAGATTTTGGAGAGAGATG--GTTTTTGGCATGAGNAITGAGGGCCAAACCAA	508 			
OY	2294 GAGTCAGGCCCTTAATTTTCATTAATTTAACTCAGAGGGGAAAGTAATATTTCAGGCA	2353 			
Dd	509 CAGTAGGCACTTAATGCGCACGTATACTAAGCTTCAGAGACAAAGTAATATTTCAGGCA	568 			
OY	2354 TACTGACACTTTGCCA	2369 			
Dd	569 TCCTACTACTTTATCA	584 			

```

RESULT 7
US-09-755-633-6/c
; Sequence 6, Application US/09755633
; Patent No. US20020127200A1
; GENERAL INFORMATION:
; APPLICANT: Yang, Shumin
; APPLICANT: McCall, Catherine A.
; APPLICANT: Weber, Eric R.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF
; FILE REFERENCE: IM-2-C1-C1
; CURRENT APPLICATION NUMBER: US/09/755,633
; CURRENT FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: 09/322,409
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/087,306
; PRIOR FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 610
; TYPE: DNA
; ORGANISM: Canis familiaris
'us-09-755-633-6

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Query Match	4.78;	Score 152.4;	DB 10;	Length 610;
Best Local Similarity	77.38;	Pred. No. 9e-21;		
Matches. 198;	Conservative	0;	Mismatches 56;	Indels 2;
				Gaps 1;
QY 2114	ACAGAAAAAGTGTGCGAGAGAAAGACGAGAGATAAACCAATTCTAGACTACCTGCAAGA	2173		
Db 280	AAAAAAAAGGTGCGAGAGAAAGATGAGAGTGACAAAGTTCCTAGACTACCTGCAAGT	221		
QY 2174	GTTTCTTGGTGAATGAACACCGAGTGGATTAATAGAAAGTTGAGACTAACTGGTTGTT	2233		
Db 220	ATTTCTTGTTGAATTAACACCGAGTGGACACCGGAAGTTGAGAACAAACCGGCTTATT	161		
QY 2234	GCAGCCAAAGATTTTGGAGAGAGAAGACATTTTACTGCAGTGAGAAATGAGGCCCAAGAA	2293		
Db 160	GTAGTGAAGATTTTGGAGAGAAGATG--GTTTTTTGGCGATGAGAATGAGGCCAACCAA	103		
QY 2294	GAGTCAGGCCTTAATTTTCAATATAATTAACTTCAGAGGGAAGTAATATTTTCAGGCA	2353		
Db 102	CAGTAGGACTTAATGGCCAGTATAACTAAGCTTCAGAGACAAAGTAATATTTTCAGGCA	43		
QY 2354	TACTGACACTTTGCCA	2369		
Db 42	TTCTACTACTTTTATCA	27		

RESULT 8

US-09-755-633-7

; Sequence 7, Application US/09755633
; Patent No. US20020127200A1

; GENERAL INFORMATION:

; APPLICANT: Yang, Shumin

; APPLICANT: McCall, Catherine A.

; APPLICANT: Weber, Eric R.

; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC

; FILE REFERENCE: IM-2-C1-C1

; CURRENT APPLICATION NUMBER: US/09/755,633

; CURRENT FILING DATE: 2001-01-05

; PRIOR APPLICATION NUMBER: 09/322,409

; PRIOR FILING DATE: 1999-05-28

; PRIOR APPLICATION NUMBER: 60/087,306

; PRIOR FILING DATE: 1998-05-29

; NUMBER OF SEQ ID NOS: 21

; SOFTWARE: Patentln Ver. 2.1

; SEQ ID NO 7

; LENGTH: 402

; TYPE: DNA

; ORGANISM: Canis familiaris

US-09-755-633-7

Query Match 3.1%; Score 99.4; DB 10; Length 402;

Best Local Similarity 75.2%; Pred. No. 2.3e-10;

Matches 124; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

QY 553 ATGAGGATGCTTCTGCATTTGAGTTGCTAGCTCTTGAGGCTGCTACGTATGCCATC 612

Db 1 ATGAGGAATGCTTCTGCAATTTGAGTTGCTAGCTCTTGAGGCTGCTACGTATGCCATC 60

QY 613 CCCACAGAAATTCACAGAGTGCATGCTGAAAGAGACCTGGCAGCTGCTTCTACTCAT 672

Db 61 GCTGTAGAAAATCCCATGATGATGAGTGGCAGAGACCTTGACACTGCTCTCCACTCAT 120

QY 673 CGAAGCTGCTGATAGCCCAATGAGGTAATTTCTTTATGATTCCT 717

Db 121 CGAAGCTGCTGATAGCCCAATGAGGTAATTTCTTTATGATTCCT 165

RESULT 9

US-09-755-633-8/c

; Sequence 8, Application US/09755633

; Patent No. US20020127200A1

; GENERAL INFORMATION:

; APPLICANT: Yang, Shumin

; APPLICANT: McCall, Catherine A.

; APPLICANT: Weber, Eric R.

; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC

; FILE REFERENCE: IM-2-C1-C1

; CURRENT APPLICATION NUMBER: US/09/755,633

; CURRENT FILING DATE: 2001-01-05

; PRIOR APPLICATION NUMBER: 09/322,409

; PRIOR FILING DATE: 1999-05-28

; PRIOR APPLICATION NUMBER: 60/087,306

; PRIOR FILING DATE: 1998-05-29

; NUMBER OF SEQ ID NOS: 21

; SOFTWARE: Patentln Ver. 2.1

; SEQ ID NO 8

; LENGTH: 402

; TYPE: DNA

; ORGANISM: Canis familiaris

US-09-755-633-8

Query Match 3.1%; Score 99.4; DB 10; Length 402;

Best Local Similarity 75.2%; Pred. No. 2.3e-10;

Matches 124; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

QY 553 ATGAGGATGCTTCTGCATTTGAGTTGCTAGCTCTTGAGGCTGCTACGTATGCCATC 612

Db 402 ATGAGGAATGCTTCTGCAATTTGAGTTGCTAGCTCTTGAGGCTGCTACGTATGCCATC 343

QY 613 CCCACAGAAATTCACAGAGTGCATGCTGAAAGAGACCTGGCAGCTGCTTCTACTCAT 672

Db 342 GCTGTAGAAAATCCCATGATGATGAGTGGCAGAGACCTTGACACTGCTCTCCACTCAT 283

QY 673 CGAAGCTGCTGATAGCCCAATGAGGTAATTTCTTTATGATTCCT 717

Db 282 CGAAGCTGCTGATAGCCCAATGAGGTAATTTCTTTATGATTCCT 238

RESULT 10

US-09-755-633-9

; Sequence 9, Application US/09755633

; Patent No. US20020127200A1

; GENERAL INFORMATION:

; APPLICANT: Yang, Shumin

; APPLICANT: McCall, Catherine A.

; APPLICANT: Weber, Eric R.

; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC

; FILE REFERENCE: IM-2-C1-C1

; CURRENT APPLICATION NUMBER: US/09/755,633

; CURRENT FILING DATE: 2001-01-05

; PRIOR APPLICATION NUMBER: 09/322,409

; PRIOR FILING DATE: 1999-05-28

; PRIOR APPLICATION NUMBER: 60/087,306

; PRIOR FILING DATE: 1998-05-29

; NUMBER OF SEQ ID NOS: 21

; SOFTWARE: Patentln Ver. 2.1

; SEQ ID NO 9

; LENGTH: 345

; TYPE: DNA

; ORGANISM: Canis familiaris

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (1)..(345)

US-09-755-633-9

Query Match 2.8%; Score 90.2; DB 10; Length 345;

Best Local Similarity 76.9%; Pred. No. 1.4e-08;

Matches 110; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

QY 1881 AGCAACCACTGTGCACATGAGAAATCTTTCAGGGAATAGGCACACTGGAGAGTCAACTG 1940

Db 119 ATCAACCACTGTGCATTAAGAAGTTTTCAGGGATAGACACATTTGAAGAACCAACTG 178

QY 1941 TGCAGGGGGTACTGTGGAAGACTATTCAAAACCTGCTTATATTAAGAAATACATG 2000

Db 179 CCCAGGGGAGGCTGTGATTAACCTATTCAAAACCTGCTTATATTAAGAAACACATAG 238

QY 2001 ACGGCCAAAAGTAAGTTACCA 2023

Db 239 AGCGCCAAAAGTAAGTTGCA 261

RESULT 11

US-09-755-633-11/c

; Sequence 11, Application US/09755633

; Patent No. US20020127200A1

; GENERAL INFORMATION:

; APPLICANT: Yang, Shumin

; APPLICANT: McCall, Catherine A.

; APPLICANT: Weber, Eric R.

; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC

; FILE REFERENCE: IM-2-C1-C1

; CURRENT APPLICATION NUMBER: US/09/755,633

; CURRENT FILING DATE: 2001-01-05

; PRIOR APPLICATION NUMBER: 09/322,409

; PRIOR FILING DATE: 1999-05-28

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; TITLE OF INVENTION: Nucleic Acids, proteins, and Antibodies
;
; FILE REFERENCE: PC009
;
; CURRENT APPLICATION NUMBER: US/09/764,847
;
; CURRENT FILING DATE: 2001-01-17
;
; Prior application data removed - consult PALM or file wrapper

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; NUMBER OF SEQ ID NOS: 2003
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1549
; LENGTH: 32193
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-847-1549

Query Match 1.9%; Score 61; DB 10; Length 32193;
Best Local Similarity 61.8%; Pred. No. 0.066;
Matches 97; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

QY 1706 ACTTTGTGGACCAAAATGTTTAAATAATTTTAAATTGATGAATTAAAGTATAT 1765
||||| | | | | | | | | | | | | | | | | |
DB 9368 ACTTCTAATACACACAGCAGTGTCTTTGTTATTTAAGCTGACAAATPAAAAATTGTAT 9427
QY 1766 ATATTTATTTGCTACATATGATGTTTGAAGTATGTATACATTGCAGATGACAAATG 1825
||||| | | | | | | | | | | | | | | | | |
DB 9428 ATATTTATGCTACACATGATGTTTGAATATATGTATACGTTGTGGAATGTTAACAA 9487
QY 1826 ACCAAATTTTATACCTTGTCTTGATTTTGCATTT 1862
| | | | | | | | | | | | | | | | | |
DB 9488 GCTAATTAGCAATTAACATCACAATACCTTTT 9524

Search completed: April 24, 2003, 03:46:30
Job time : 458 secs

